

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:26:15 ; Search time 7703 Seconds
(without alignments)
10939.950 Million cell updates/sec

Title: US-10-765-580-11

Perfect score: 1507
Sequence: 1 atgacacatcatcatcatca.....gtgacaagccagcgctga 1507

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

RST:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	33.0	510	14 AY407604	AY407604 Homo sapi
2	484.6	32.2	988	6 BX442364	BX442364 BX442364
3	484.4	32.1	3562	6 BC058855	BC058855 Homo sapi
4	421.8	26.0	520	9 DN350259	DN350259 LIBS579-0
5	400	26.5	510	14 AY407605	AY407605 Pan trogl
6	370.2	24.6	828	8 CO886262	CO886262 Boygen_14
7	363.6	24.1	485	14 AY407606	AY407606 Mus muscu
8	344	22.8	535	9 AU279816	AU279816 AU279816
9	344	22.8	547	1 AU279816	AU279816 AU279816
10	327.2	21.7	791	5 CK364171	CK364171 AGENCOURT
11	326.8	21.7	528	3 BO674897	BO674897 AGENCOURT
12	323.2	21.4	890	2 BI869727	BI869727 603393614
13	323.2	21.4	600	3 BU919454	BU919454 6023-75 M
14	322.2	20.8	1683	6 CR614384	CR614384 full-length
15	314	20.7	459	1 AI591060	AI591060 tw28f02.x
16	312.4	20.6	752	4 CA505431	CA505431 UI-R-FSI-
17	296	19.3	953	3 BO713895	BO713895 AGENCOURT
18	291.4	19.3	904	4 BX426783	BX426783 BX426783
19	285	18.9			

20	276	18.3	558	9 DA172761	DA172761 DA172761
21	268	17.8	799	5 CK465017	CK465017 936084 MA
22	261.6	17.4	752	3 BO780197	BO780197 UI-R-EP0
23	261	17.3	613	3 BO832724	BO832724 L6in2102
24	261	17.3	803	9 CX898524	CX898524 JGI_CAM8
25	260	17.3	490	4 CB725648	CB725648 AMGNNUC:M
26	254.4	16.9	726	8 CX009700	CX009700 i042b10.g
27	249.8	16.6	495	4 BX445267	BX445267 BX445267
28	248.8	16.5	543	2 BG311141	BG311141 i455c02.y
29	241	16.0	632	5 CK479447	CK479447 AGENCOURT
30	235.4	15.6	920	3 BU848858	BU848858 AGENCOURT
31	234.8	15.5	777	5 CK367183	CK367183 AGENCOURT
32	227.8	15.1	600	3 BF514775	BF514775 UI-H-BM1-
33	227.8	15.1	924	3 BU153227	BU153227 UI-R-EP0-
34	227.6	15.1	874	3 BO208280	BO208280 UI-R-EP0-
35	225.8	15.0	887	3 BO959864	BO959864 AGENCOURT
36	223.6	14.8	689	3 BO199378	BO199378 UI-R-EB0-
37	222.2	14.7	601	8 CX234175	CX234175 MEM16055
38	217.2	14.4	639	10 DT887832	DT887832 1464547 M
39	217	14.4	442	7 AM141848	AM141848 EST291963
40	214	14.2	301	7 BE165543	BE165543 OVO-HT049
41	207.2	13.7	600	2 BG803325	BG803325 0223-76 M
42	204	13.5	534	3 BM991154	BM991154 UI-H-D10-
43	203.2	13.5	649	7 BF679862	BF679862 602154448
44	199.6	13.2	244	2 BF841362	BF841362 RC2-HT107
45	195	12.9	521	7 AM630808	AM630808 hh87h03.y

ALIGNMENTS

RESULT 1	AY407604	510 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY407604				
DEFINITION	Homo sapiens VEGF gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY407604.1	GI:39763575			
VERSION	AY407604.1	GI:39763575			
KEYWORDS	GSS.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 510)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
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	/gene="VEGF"				
	/locus_tag="HCM2946"				

CONSRMT
TITLE
JOURNAL
REFERENCE
AUTHORS
CONSRMT
TITLE
JOURNAL
REMARK
COMMENT

Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Cassavatt, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Kana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McEwan, K.C., Malek, J.A., Guaratine, P.H., Richards, S.W., Woley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hultky, S.M., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Nadeau, A., Young, A.C., Shchepochenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buetefield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

2 (bases 1 to 3562)

NIH MGC Project
Direct Submission
Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk

FEATURES

Tissue Procurement: Miklos Patkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amgdbcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lougheseg, H.,
Kovits, C.R., Snead, A.J., Martin, R.G., Muzny, D.M., Nannavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Series: IRAK Plate: 91 Row: n Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 71051577
This clone has the following problem: frame shifted.
Location/Qualifiers

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1. .3562
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				Indels	1
				Gaps	1

Db	1234	GATGAGATTCGATGATCAATCTTTCAAGGCATCTGTGTGGCCCTTAATGCGATCGGGGGCGTC	1293
Qy	1190	TGCAATGACGAGGGCCCTGGAGTGTGTGCCCCATCTGAGAGTCCAAACATCACCATGCGAGATT	1249
Db	1294	TGCAATGACCAAGGGCCCTGGAGTGTGTGCCCATCTGAGAGTCCAAACATCACCATGCGAGATT	1353
Qy	1250	ATGGCGATTCGAACCTTCACAAAGGCACGACATAGAGAGATGAGCTTCTTACGACACAC	1309
Db	1354	ATGGGGAATCAAACTTCACAAAGGCACGACATAGAGAGATGAGCTTCTTACGACACAC	1413
Qy	1310	AAATGTGATATGACAGCCMAAGAAAGATAGACAAACAAGAAAATCCCTGTGGGCTTTGC	1369
Db	1414	AAATGTGATATGACAGCCMAAGAAAGATAGACAAACAAGAAAATCCCTGTGGGCTTTGC	1473
Qy	1370	TCAGAGCGGAGAAAGCATTTGTTGTTGTAACAAGATCCCGACAGCTGTAAATGTTCCCTGCAA	1429
Db	1474	TCAGAGCGGAGAAAGCATTTGTTGTTGTTACAAGATCCCGACAGCTGTAAATGTTCCCTGC-AA	1532
Qy	1430	AAACAACAATCCGCTTCACAGGCGCAGGACGCTTGATTTAAACGAACCTAATTGACAGATGT	1489
Db	1533	AAACAACAATCCGCTTCACAGGCGCAGGACGCTTGATTTAAACGAACCTAATTGACAGATGT	1592
Qy	1490	GACAAGCGGAGGCGGTGA	1507
Db	1593	GACAAGCGGAGGCGGTGA	1610

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RESULT 4
DN350259
LOCUS
DEFINITION DN350259 520 bp mRNA linear EST 04-MAR-2005
LIB3579-026-01-K1-H10 LIB3579 Canis familiaris cDNA clone
CIN2484766, mRNA sequence.
ACCESSION DN350259
VERSION DN350259.1 GI:60522951
KEYWORDS
SOURCE
ORGANISM
EST.
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 520)
Staten,N.R.
Direct Submission (Staten,N.R.)
Unpublished (2005)
JOURNAL
Contact: Nick Staten
COMMENT
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
FEATURES
1
520
location/Qualifiers

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1: 520
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control dog"

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			Gaps	0
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Db	40	CCAGGCTGCGCCTATGCGCAGAGAGAGACCAACCCTCAGAAAGTGTGAAGTTATGGA	99	
QY	1066	TGTTTATTCAGCGCAGACTATGCGATTCATTCGACGACCTGTGTGACATCTTCAGAGATTA	1122	
Db	100	CGTTTACAGCGCAGACTATGCGCGCTCCATTGAGACCTGTGTGACATCTTCAGAGATTA	159	

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 DB 520 A 520
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RESULT 5
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 LOCUS Pan troglodytes VEGF gene, VIRUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 AY407605
 ACCESSION AY407605.1 GI:39763576
 VERSION
 KEYWORDS
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Pan

REFERENCE
 AUTHORS 1 (bases 1 to 510)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
 Perrieria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 510)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
 Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
 Perrieria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment

FEATURES
 Location/Qualifiers
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 DB 133 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCCCTGATGCGAGGGCTGC 192
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 DB 193 TGCATGACGAGGCGCTGAGAGTGTGTGCCCCCTGATGAGAGTCCAACTACCATGACAT 252
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 DB 373 TCAGAGCGGAGAAAGCATTTTGTGTGTCAAGATCCGACGATGTAATGTTCTGCAAA 432
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 DB 433 NNN 492
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 DB 493 GACAGCCGAGGCGGTGA 510
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RESULT 6
 CO886262 828 bp mRNA linear EST 01-SEP-2004
 LOCUS Bovgen.14587 normal cattle brain Bos taurus cDNA clone
 DEFINITION RZP01056P0311Q 5', mRNA sequence.
 CO886262
 ACCESSION CO886262.1 GI:51816547
 VERSION
 KEYWORDS
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos

REFERENCE
 AUTHORS 1 (bases 1 to 828)
 Hennig,S., Janitz,M., Herwig,R. and Williams,J.
 Generation, annotation, evolutionary analysis and database
 integration of 14969 cattle EST clusters
 JOURNAL unpublished (2004)
 COMMENT
 Contact: Hennig S
 Laboratory 123, dep. Lehrach
 Max-Planck-Institut fuer Molekulare Genetik
 Ihnestr.63-73, D-14195 Berlin, Germany
 Tel: +49 30 8413 1612
 Fax: +49 30 8413 1380
 Email: hennig@molgen.mpg.de
 The library was characterised by oligonucleotide fingerprinting
 (ONFP) to reduce sequencing redundancy. According to the ONFP
 procedure, clones that display the same hybridisation matrix with a
 battery of 200 8mer oligonucleotides are grouped into clusters. One
 clone per ONFP cluster was selected for sequencing. cDNA clones and
 filters are distributed via Deutsches Ressourcenzentrum fuer
 Genomforschung GmbH (http://www.rzpd.de).

PCR Primers
 FORWARD: 5' CCCGAGCTTACACTTATGTTCCGGCTCG 3' (M13RSP) 5'-seq

TITLE

JOURNAL
PUBMED
COMMENT

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Iishi, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N., Yonekawa, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Magatsuma, M., Morikawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification and Characterization of Putative Alternative Identification and Characterization of Putative Alternative Promoters of Human Genes Genome Res. 16 (1), 55-65 (2006)

16344560

Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com

NEDO human CDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB

FEATURES

source

Location/Qualifiers
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ORIGIN

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QY 1010 GCACCCATGGCAGAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTGATGATGTC 1069
DB 173 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTGATGATGTC 232
QY 1070 TATACGCGAGCTACTGCCATCCATGAGACCTGTGTGACATCTTCGAGGATACCT 1129
DB 233 TATACGCGAGCTACTGCCATCCATGAGACCTGTGTGACATCTTCGAGGATACCT 292
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DB 293 GATGAGATCGAGTACATCTTCAGCCATCTGTGTGCTGATGCGATCGGGGCTGC 352
QY 1190 TGCATGACGAGGCGCTGTGAGTGTGCCACTGAGAGTTCACATCAGATGATTT 1249
DB 353 TGCATGACGAGGCGCTGTGAGTGTGCCACTGAGAGTTCACATCAGATGATTT 412
QY 1250 ATGGGATCAAACTCCACCAAGGCGCAGACATAGAGAGATGACCTTCACACACAC 1309
DB 413 ATGGGATCAAACTCCACCAAGGCGCAGACATAGAGAGATGACCTTCACACACAC 472
QY 1310 AAATGTGATGACAGACCAAGAAAGATAGACCAAGCAAGAAAA 1353
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RESULT 9
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LOCUS AU279816 CHONS2 Homo sapiens cDNA clone CHONS2001577 5', mRNA
DEFINITION
ACCESSION AU279816
VERSION AU279816.1 GI:28299043
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 547)
Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R., Isogai, T., Hata, J., Tomoya, Y. and Umezawa, A.
Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis Exp. Cell Res. 288 (1), 35-50 (2003)

12878157

Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com

HRI human CDNA Project, Sugiyama, T.; Makamatsu, A.; Irie, R.; Umezawa, A.; Fukuma, M.; Kusakari, S.; Hata, J.; Iishi, S.; Yamamoto, J.; Isono, Y.; Saito, K.; Nakamura, Y.; Masuno, Y.; Nagai, K.; Isogai, T.
HRI human CDNA Project; cDNA library construction & 5'-end one pass sequencing: Helix Research Institute.

FEATURES

source

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/note="Vector: PME18SFL3"

ORIGIN

Query Match 22.8%; Score 344; DB 1; Length 547;
Best Local Similarity 100.0%; Pred. No. 6.9e-92; Indels 0; Gaps 0;
Matches 344; Conservative 0; Mismatches 0;

QY 1010 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTGATGATGTC 1069
DB 6 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAGTGTGAAGTTGATGATGTC 65
QY 1070 TATACGCGAGCTACTGCCATCCATGAGACCTGTGTGACATCTTCGAGGATACCT 1129
DB 66 TATACGCGAGCTACTGCCATCCATGAGACCTGTGTGACATCTTCGAGGATACCT 125
QY 1130 GATGAGATCGAGTACATCTTCAGCCATCTGTGTGCTGATGCGATCGGGGCTGC 1189
DB 126 GATGAGATCGAGTACATCTTCAGCCATCTGTGTGCTGATGCGATCGGGGCTGC 185
QY 1190 TGCATGACGAGGCGCTGTGAGTGTGCCACTGAGAGTTCACATCAGATGATTT 1249
DB 186 TGCATGACGAGGCGCTGTGAGTGTGCCACTGAGAGTTCACATCAGATGATTT 245
QY 1250 ATGGGATCAAACTCCACCAAGGCGCAGACATAGAGAGATGACCTTCACACACAC 1309
DB 246 ATGGGATCAAACTCCACCAAGGCGCAGACATAGAGAGATGACCTTCACACACAC 305
QY 1310 AAATGTGATGACAGACCAAGAAAGATAGACCAAGCAAGAAAA 1353
DB 306 AAATGTGATGACAGACCAAGAAAGATAGACCAAGCAAGAAAA 349

RESULT 10
BX443079 880 bp mRNA linear EST 04-MAY-2004
LOCUS BX443079 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
DEFINITION
ACCESSION BX443079
VERSION BX443079.2 GI:47001997
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 880)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30774104.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 3853.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0D004AD02QPl&c=3853.f.

FEATURES

source

1. 880
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D004YG03"
/tissue_type="B CELLS (RAMOS CELL LINE)"
/cell_line="RAMOS CELL LINE"
/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 21.7%; Score 327.2; DB 4; Length 880;
Best Local Similarity 98.0%; Pred. No. 9.8e-87;
Matches 337; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

1010 GGACCCATGGAGAGAGAGAGAGAGAGATCATCATCGAAGTGTGAAGTTTCATGATGTC 1069
538 GACCCATGGAGAGAGAGAGAGAGATCATCATCGAAGTGTGAAGTTTCATGATGTC 597
1070 TATCAGCGAGCTACTGCTCATCATCGAGACCTGTGTGAGATCTTCCAGAGTACCT 1129
598 TATCAGCGAGCTACTGCTCATCATCGAGACCTGTGTGAGATCTTCCAGAGTACCT 1129
1130 GATGAGATCGAGTACTCTTCAAGCATCTGTGTGCTGCTGATGCGATGCGGGGCTGC 1189
657 GATGAGATCGAGTACTCTTCAAGCATCTGTGTGCTGCTGATGCGATGCGGGGCTGC 716
1190 TGCATGAT 1249
717 TGCATGAT 776
1250 ATGCGGATCAAACTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1309
777 ATGCGGATCAAACTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 836
1310 AAATGTGAATGACAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1353
837 AAATGTGAATGACAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 880

RESULT 11
CK364171 791 bp mRNA linear EST 23-Dec-2003
LOCUS CK364171
DEFINITION AGENCOURT_17158461 NIH_MGC_231 Rattus norvegicus cDNA clone
IMAGE:7096576 5', mRNA sequence.
ACCESSION CK364171
VERSION CK364171.1 GI:40330106
KEYWORDS EST.

SOURCE
ORGANISM

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 791)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM14941 row: h column: 14
High quality sequence stop: 690.
Location/Qualifiers

FEATURES

source

1. 791
Location/Qualifiers

/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7096576"
/tissue_type="lung, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_231"
/note="Organ: lung; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from pooled lung tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
5'-pGACTGATGTTTCAGTACGCGAGCGCGCCGCTT25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.3 kb. This primary library is not normalized (normalized primary library is NIH MGC 232) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

Query Match 21.7%; Score 326.8; DB 5; Length 791;
Best Local Similarity 77.4%; Pred. No. 1.2e-86;
Matches 443; Conservative 0; Mismatches 57; Indels 72; Gaps 1;

1008 AGGACCCATGGAGAGAGAGAGAGAGAGATCATCATCGAAGTGTGAAGTTTCATGATG 1067
1 AGGCTGCACCCACGACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 60
1068 TCTATCAGAT 1127
61 TTTACACAGAT 120
1128 CTGATGAGATGAGTACATCTTCAAGCATCTGTGTGCTGCTGATGCGAGTGGGGCT 1187
121 CCGATGAGTATGATATCTTCAAGCGCTCTGTGTGCTGCTTAAATGCGGTGTGGGGCT 180
1188 GCTGCAATGACAGAT 1247
181 GCTGCAATGATGAT 240
1248 TTATGCGATCAAACTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1307
241 TCAATGAGATCAAACTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 300
1308 ACAATGTGAATGACAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1353
301 GCAGATGTGAATGACAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 360

QY 1354 -----TC 1355
Db 361 GAAAGGAAAGGGTCAAAAAGCAAGCCAGAAATCCCGGTTTAAATCTGAGCGTTC 420
QY 1356 CCTGTGGGCTTGTCTCAGAGCGGAGAAAGCATTTTGTGTACAGATCCGAGACGTGTA 1415
Db 421 ACTGTAGGCTTGTCTCAGAGCGGAGAAAGCATTTTGTGTCCAAATCCGAGACGTGTA 480
QY 1416 AATGTTCTGCAAAAACACAGACTGCGGTTGCAAGCGGAGCGAGCGTGTAAACGAC 1475
Db 481 AATGTTCTGCAAAAACACAGACTGCGGTTGCAAGCGGAGCGAGCGTGTAAACGAC 540
QY 1476 GTACTTGACAGATGTGACAAAGCCAGGCGGTGA 1507
Db 541 GTACTTGACAGATGTGACAAAGCCAGGCGGTGA 572
RESULT 12
BO674897 528 bp mRNA linear EST 15-JUL-2002
LOCUS BO674897
DEFINITION AGENCOURT 8036450 NIH_MGC_102 Homo sapiens CDNA clone IMAGE:6212223
5' mRNA sequence.
ACCESSION BO674897
VERSION BO674897.1 GI:21785731
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 528)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2375 row: p column: 16
High quality sequence stop: 527.
Location/Qualifiers
1. 528
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6212223"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 102"
/note="Organ: salivary gland; Vector: pOT7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.4%; Score 323.2; DB 3; Length 528;
Best Local Similarity 96.2%; Pred. No. 1.3e-85;
Matches 331; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGGCGCAGATCATACGAGATGTTGAAGTTTCATGATGTC 1069
Db 174 GCACCCATGCGAGAGAGAGGCGCAGATCATACGAGATGTTGAAGTTTCATGATGTC 233

QY 1070 TATCAGGCGAGCTACTGCTCCATCCATGAGAGACCCCTGGTGACATCTTCCAGAGTACCT 1129
Db 234 TATCAGGCGAGCTACTGCTCCATCCATGAGAGACCCCTGGTGACATCTTCCAGAGTACCT 293
QY 1130 GATGAGATGAGTACATCTTCAAGCCATCTGTGTGCTCCCTGATGCGATGCGGGGCTGC 1189
Db 294 GATGAGATGAGTACATCTTCAAGCCATCTGTGTGCTCCCTGATGCGATGCGGGGCTGC 353
QY 1190 TGCATATACAGAGGCTTGTGATGTGTGCTCCAGTGGAGATCCAAATCACATGACAGATT 1249
Db 354 TGCATATACAGAGGCTTGTGATGTGTGCTCCAGTGGAGATCCAAATCACATGACAGATT 413
QY 1250 ATGCGATCAAACTCTCAGAGGCGAGACATGAGAGATGAGCTTCTTACAGACAC 1309
Db 414 ATGCGATCAAACTCTCAGAGGCGAGACATGAGAGATGAGCTTCTTACAGACAC 473
QY 1310 AATGTGAAATGACAGACCAAGAAAGATGAGACAGACAGACAAA 1353
Db 474 AATGTGAAATGACAGACCAATTAAGTTAAATGAGAAAAAA 517
RESULT 13
B1869727 890 bp mRNA linear EST 11-OCT-2001
LOCUS B1869727
DEFINITION 603393614P1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:5403771 5',
mRNA sequence.
ACCESSION B1869727
VERSION B1869727.1 GI:16043400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 890)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM12029 row: k column: 04
High quality sequence stop: 733.
Location/Qualifiers
1. 890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5403771"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NcoI;
Site_2: SalI; cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.4%; Score 323.2; DB 2; Length 890;
Best Local Similarity 99.1%; Pred. No. 1.6e-85;
Matches 325; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1058 TTTCATGATGTCATATCAGGCGACCTACTGCGATTCATCAGACCTGTGTGACATCTTC 1117
Db 1 TTTCATGATGTCATATCAGGCGACCTACTGCGATTCATCAGACCTGTGTGACATCTTC 60

[illegible]

Db	1201	GGGGCTGGATGTGTGTGCCCACTAGAGTCCAAATCATCAGATGAGATTTCGGAATCAA	1250
QY	1261	ACCTTCACCAAGGCCACAGACATATGAGAGAGATGAGTTCCTTCACAGACAACAATATGTAAATG	1320
Db	1261	ACCTTCACCAAGGCCACAGACATATGAGAGAGATGAGTTCCTTCACAGACAACAATATGTAAATG	1320
QY	1321	CAGACCCAAGAAAGATAGAGCAACAAGAAATCCCTGTGGGCTTGTCTCAGAGCCGAG	1380
Db	1321	CAGACCCAAGAAAGATAGAGCAACAAGAAATCCCTGTGGGCTTGTCTCAGAGCCGAG	1380
QY	1381	AAAGCATTTGTTTGTACAAGATCCGAGAGGTGTAAATGTTCCTCGCAAAAAACACAGACTC	1440
Db	1381	AAAGCATTTGTTTGTACAAGATCCGAGAGGTGTAAATGTTCCTCGCAAAAAACACAGACTC	1440
QY	1441	GGCGTTGCACAGGCGAGGCGAGCTTGAATTAAAGAAAGCTACTTGCAGATGTGCAAGCCGAG	1500
Db	1441	GGCGTTGCACAGGCGAGGCGAGCTTGAATTAAAGAAAGCTACTTGCAGATGTGCAAGCCGAG	1500
QY	1501	GGCGGTGA 1507	
Db	1501	GGCGGTGA 1507	

RESULT 2

US-09-334-477-46
; Sequence 46, Application US/09334477
; Patent No. US20020012658A1

GENERAL INFORMATION:

APPLICANT: Williams, James A.

Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco
STATE: California

COUNTRY: United States of America

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM:
SOFTWARE: Patent T

CURRENT APPLICATION DATA: HC/00/234 477

FILING DATE: 16-Jun-2017

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;
; .CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: 100-443887
FILING DATE: 01/11/2011

ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Karmir

REGISTRATION NUMBER

REFERENCE/DOCKET NUMBER: OPHD-02450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 391-1111
TELEFAX: (415) 391-1111

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:

LENGTH: 2073 base

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; TYPE: nucleic acid
; STRANDEDNESS: double

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;
; TOPOLOGY: linear
MOLECULE TYPE: other n

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DESCRIPTION: /desc = "DNA"
FEATURE:
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NAME/KEY:	CDS
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; LOCATION: 1..2070
; SEQUENCE DESCRIPTION: SEQ ID NO: 46::

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US-09-334-477-46

Query Match 58.5%; Score 881.4; DB 3; Length 2073;
 Best Local Similarity 99.3%; Pred. No. 1.3e-260;
 Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

99 CCCGATCTGAGGAAATTTACCTTACGATCTTCGACCTGCAAAAGCAGTATGATTTGGCT 158
 1182 CCCGAAATTTCAAGGAAATTTACCTTACGATCTTCGACCTGCAAAAGCAGTATGATTTGGCT 1241
 159 GAATGTCATCTGCTGCAATAGGACTCCATTCACAGCTATTCATCAGAGGATGCTC 218
 1242 GAATGTCATCTGCTGCAATAGGACTCCATTCACAGCTATTCATCAGAGGATGCTC 1301
 219 TTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
 1302 TTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1361
 279 AGATTCAG 338
 1362 AGATTCAG 1421
 339 TGTGACAGATTTGTTAAG 398
 1422 TGTGACAGATTTGTTAAG 1481
 399 TGTGACAGATTTGTTAAG 458
 1482 TGTGACAGATTTGTTAAG 1541
 459 ACAGCGGTTGCAAGGATTCATGTCGAGGAGATGAGATTAATGCGCATTTGGTACATC 518
 1542 ACAGCGGTTGCAAGGATTCATGTCGAGGAGATGAGATTAATGCGCATTTGGTACATC 1601
 519 TTCTTATCTGATTTAATGTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
 1602 TTCTTATCTGATTTAATGTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1661
 579 GATGTTACGTTGTTGTTAAG 638
 1662 GATGTTACGTTGTTGTTAAG 1721
 639 ATTGTCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
 1722 ATTGTCGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1781
 699 TGATCTTACATTTGAAG 758
 1782 TGATCTTACATTTGAAG 1841
 759 CTCTGTTGCTGAG 818
 1842 CTCTGTTGCTGAG 1901
 819 ATTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
 1902 ATTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1961
 879 TCCTTCTATGTCGCGAG 938
 1962 TCCTTCTATGTCGCGAG 2021
 939 GGATTCATCCACTCTGGGGGCAATTTCTATGCGGCAAACTATTAGCACTG 989
 2022 GGATTCATCCACTCTGGGGGCAATTTCTATGCGGCAAACTATTAGCACTG 2072

489

RESULT 3
 US-09-334-477-32
 ; Sequence 32, Application US/09334477
 ; Patent No. US20020012658A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, James A.
 ;
 ; Byrne, Lisa M.

Pugh, Charles S.G.
 TITLE OF INVENTION: Prevention And Treatment Of
 Verotoxin-Induced Disease
 NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Medien & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/334,477
 FILING DATE: 16-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/816,977
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: MacKnight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2127 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..2127
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 US-09-334-477-32

Query Match 58.4%; Score 879.4; DB 3; Length 2127;
 Best Local Similarity 99.3%; Pred. No. 5.6e-260;
 Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

101 CAGATCGAAGAGATTTACCTTACGATCTTCGACCTGCAAAAGCAGTATGATTCGCTGA 160
 1238 CAGAAATTCAGAAATTTACCTTACGATCTTCGACCTGCAAAAGCAGTATGATTCGCTGA 1297
 161 ATGTCATCTGCTGCAATAGGATCTCCATTACAGACTATTTCATCAGAGGATGCTTT 220
 1298 ATGTCATCTGCTGCAATAGGATCTCCATTACAGACTATTTCATCAGAGGATGCTTT 1357
 221 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 280
 1358 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1417
 281 ATCCAG 340
 1418 ATCCAG 1477
 341 TGACAGATTTGTTAAG 400
 1478 TGACAGATTTGTTAAG 1537
 401 TTACTTTCAGAGTACACAG 460
 1538 TTACTTTCAGAGTACACAG 1597
 461 AGCGTTGCAAGGATCAGTCTGACGGGAGATGAGATTAATGCGCATTTGGTACTT 520

Db	1598	AGCGGTTGACAGGAGATCACTGGTACGGGGATGACAGATTAATCCGCAATTCGTTGACTACTT	1657
Oy	521	CTTATCTCGGATTTAAATGTCGCATAGTGGAACTCATCCAGCAGCTCTGTGGCAAGACGA	580
Db	1658	CTTATCTCGGATTTAAATGTCGCATAGTGGAACTCATCCAGCAGCTCTGTGGCAAGACGA	1717
Oy	581	TGTTACGGTTTGTTATCTGTGACAGCTGAAGCTTTACGTTTTCGGCAATACAGAGGGAT	640
Db	1718	TGTTACGGTTTGTTATCTGTGACAGCTGAAGCTTTACGTTTTCGGCAATACAGAGGGAT	1777
Oy	641	TTTCGTACAACTGSGATGATCTCAGTGGGCGTTCTTATGTAAATGATCTGTAAGATGTTG	700
Db	1778	TTTCGTACAACTGSGATGATCTCAGTGGGCGTTCTTATGTAAATGATCTGTAAGATGTTG	1837
Oy	701	ATCTTACATTTGAACCTGGGGAAGGTTGAGTAGCGCTCTCGTCGATCATATGAGCAACAAGCT	760
Db	1838	ATCTTACATTTGAACCTGGGGAAGGTTGAGTAGCGCTCTCGTCGATCATATGAGCAACAAGCT	1897
Oy	761	CTGTTCTGTGAGAGAAATTTCTTTTGGAAAGCATTAATGCAATTTCTGGAAACGCTGGCAT	820
Db	1898	CTGTTCTGTGAGAGAAATTTCTTTTGGAAAGCATTAATGCAATTTCTGGAAACGCTGGCAT	1957
Oy	821	TAAATCTGAATGTGATCATCATCATGCGACGAGTTGCCGAATGSCATCTGATGAGTTTC	880
Db	1958	TAAATCTGAATGTGATCATCATCATGCGACGAGTTGCCGAATGSCATCTGATGAGTTTC	201
Oy	881	CTTCTATGTGTCGGCAGATGGAAAGTCCGTGGGATTAACGACAAATTAATATTTGTGGG	940
Db	2018	CTTCTATGTGTCGGCAGATGGAAAGTCCGTGGGATTAACGACAAATTAATATTTGTGGG	2077
Oy	941	ATTATATCACTCTGGGGGCAATTCGTATCGGAGAACTATTAGCAGTGG	989
Db	2078	ATTATATCACTCTGGGGGCAATTCGTATCGGAGAACTATTAGCAGTGG	2126

```

RESULT 4
US-10-765-580-9
; Sequence 9, Application us/10765580
; Publication No. US20040166565A1
; GENERAL INFORMATION:
; APPLICANT: Backer, Marina V.
; APPLICANT: Backer, Joseph M.
; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING
; TITLE OF INVENTION: SHIG-LIKE TOXIN AND VASCULAR ENDOTHELIAL GROWTH FACTOR
; TITLE OF INVENTION: FRAGMENTS
; FILE REFERENCE: 102108-300
; CURRENT APPLICATION NUMBER: US/10/765,580
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/796,861
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/190,973
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Human
US-10-765-580-9

Query Match      58.3%; Score 879; DB 8; Length 879;
Best Local Similarity 100.0%; Pred. No. 4.4e-260;
Matches 879; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      109 AAGGAATTACTTGACTTCCTCGACCTGCAAGAGAGTAGTAGTTGGCTGAATGCATT 168
      |||
Db      1 AAGGAATTACTTGACTTCCTCGACTGCAAGAGAGTAGTAGTTGGCTGAATGCATT 60

Qy      169 GCGCTGCAATAGTAGTACTTCATTACAGACTATTTTCATCAGAGAGTAAGCTCTTTACTGATG 228
      |||
Db      61 GCGCTGCAATAGTAGTACTTCATTACAGACTATTTTCATCAGAGAGTAAGCTCTTTACTGATG 120

Qy      229 ATTGATAGTGCAACAGGGGATATTTGTTTGCAAGTTGATGTACAGAGATTAATCCACAG 288

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Db	121	ATTGATAGTGGCAACAGGGGATTAATTGTTTCAGATTGATGTCAGAGGGATGATGATCAAG	180
OY	289	GAAGGCGCGTTTAATTAATCTACGGCTTAATGTGAAACAAATTAATTATATGTGACAGA	348
Db	181	GAAGGCGCGTTTAATTAATCTACGGCTTAATGTGAAACAAATTAATTATATGTGACAGA	240
OY	349	TTGTGTAACAGACAAATATATGTTTTTATGCTTGTGATTTTTTCAATGTAACCTT	408
Db	241	TTGTGTAACAGACAAATATATGTTTTTATGCTTGTGATTTTTTCAATGTAACCTT	300
OY	409	CCAGGTACACACGCGCTTACATTTGCTGTGTGACACTAGCTATACACAGCTTACAGGTTT	468
Db	301	CCAGGTACACACGCGCTTACATTTGCTGTGTGACACTAGCTATACACAGCTTACAGGTTT	360
OY	469	GCAGGGATCAGTCGACGGGAGTGCAGATTAATGCCCATTTGCTGACTACTTCTTATCTG	528
Db	361	GCAGGGATCAGTCGACGGGAGTGCAGATTAATGCCCATTTGCTGACTACTTCTTATCTG	420
OY	529	GATTTAATGTGCGCATATGTGAACTCTCACTGACGCAAGTCTGTGCAAGCCATGTTACGG	588
Db	421	GATTTAATGTGCGCATATGTGAACTCTCACTGACGCAAGTCTGTGCAAGCCATGTTACGG	480
OY	589	TTTGTACTGTGACACGCTGAAGCTTTACGTTTGGGCAAAATACAGAGGGGATTTGCTACA	648
Db	481	TTTGTACTGTGACACGCTGAAGCTTTACGTTTGGGCAAAATACAGAGGGGATTTGCTACA	540
OY	649	ACACTGATGATCTCAGTGGGCGTTCTTATGTATGATGACTGCTGAAGATGTTGATCTTACA	708
Db	541	ACACTGATGATCTCAGTGGGCGTTCTTATGTATGATGACTGCTGAAGATGTTGATCTTACA	600
OY	709	TTGAACTGGGGAAGGTTGAGTAGCGTCTGCTGACTATCATGAGACAACTCTGTTCCG	768
Db	601	TTGAACTGGGGAAGGTTGAGTAGCGTCTGCTGACTATCATGAGACAACTCTGTTCCG	660
OY	769	GTAGGAAGAAATTTCTTTTGGAAAGCATTAATGCAATCTGSGAAGCGTGCATTAATAGT	828
Db	661	GTAGGAAGAAATTTCTTTTGGAAAGCATTAATGCAATCTGSGAAGCGTGCATTAATAGT	720
OY	829	AATTGTCATCATCATGATCGCGAGTGTGCGAATGAGCATCTGTAGATTTCTTCTATG	888
Db	721	AATTGTCATCATCATGATCGCGAGTGTGCGAATGAGCATCTGTAGATTTCTTCTATG	780
OY	889	TGTCGCGCAGATGAAAGAGTCCGTGGGATTAACGACAAATPAAATATGTGGGATTCATCC	948
Db	781	TGTCGCGCAGATGAAAGAGTCCGTGGGATTAACGACAAATPAAATATGTGGGATTCATCC	840
OY	949	ACTCTGGGGGCAATTCTGATGCGCACAACATTAATAGAGT	987
Db	841	ACTCTGGGGGCAATTCTGATGCGCACAACATTAATAGAGT	879

RESULT 5
 US-09-334-477-36
 Sequence 36, Application US/09334477
 Patent No. US20020012658A1
 GENERAL INFORMATION:
 APPLICANT: Williams, James A.
 Byrne, Lisa M.
 Pugh, Charles S.G.
 TITLE OF INVENTION: Prevention And Treatment Of
 Verotoxin-Induced Disease
 NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Medien & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible


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OY      40      ACCTTTCAGATGCAACAGCGGTATCATTTGTCGGTGCAGTAGCTATPACACGTTTAC      482
Db      361      ACCTTTCCAGTACAAACAGCGGTATCATTTGTCGGTGCAGTAGCTATPACACGTTTAC      420
OY      463      CGTGTTCCAGGGAATCAGTGTGTAACGGGGATGCAAGATAAATGCCATTGGTTGACTACTTCT      522
Db      421      CGTGTTCCAGGGAATCAGTGTGTAACGGGGATGCAAGATAAATGCCATTGGTTGACTACTTCT      480
OY      523      TATTCGATTTAATGTCGATATGTGAACCTCACTGACGGCAGTCTGTGGCAAGCGCATG      582
Db      481      TATTCGATTTAATGTCGATATGTGAACCTCACTGACGGCAGTCTGTGGCAAGCGCATG      540
OY      583      TTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCCGCAAAATPACAGAGGGCATTT      642
Db      541      TTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCCGCAAAATPACAGAGGGCATTT      600
OY      643      CGTACCAACTGTGATGATCTCAGTGGGCGTTCTTAATGTAATGACTGCTGAAGATGTTGAT      702
Db      601      CGTACCAACTGTGATGATCTCAGTGGGCGTTCTTAATGTAATGACTGCTGAAGATGTTGAT      660
OY      703      CTTTACATTGAACCTGGGGAAGTTGATATACCGTCGCCCTGACTATACATGACAAGACTCT      766
Db      661      CTTTACATTGAACCTGGGGAAGTTGATATGTCCTGCCCTGATTATCATGACCAAGACTCT      720
OY      763      GTTGCGTAGAGAAGAAATTTCTTTTGGAACATTAATGCAATTCGTGGAAAGCGTGGCATTA      822
Db      721      GTTGCGTAGAGAAGAAATTTCTTTTGGAAACATTAATGCAATTCGTGGAAAGCGTGGCATTA      780
OY      823      ATACTGAATTTGCATCATCATCATGCAATCGGAGTTGCCAGATGCAATCTGATGAGTTTCT      888
Db      781      ATACTGAATTTGCATCATCATCATGCAATCGGAGTTGCCAGATGCAATCTGATGAGTTTCT      840
OY      883      TCATATGTGTCGGGAGATGGAAGATGCCGTGGGATTAAGCAATAAATATGTGGGAT      942
Db      841      TCATATGTGTCGGGAGATGGAAGATGCCGTGGGATTAAGCAATAAATATGTGGGAT      900
OY      943      TCATCCACTCTGGGGGCAATTCGTGATGCCAGACAATATTAGACGTGG      989
Db      901      TCATCCACTCTGGGGGCAATTCGTGATGCCAGACAATATTAGACGTGG      947

RESULT 7
US-10-114-170-137/c
; Sequence 137, Application US/10114170
; Publication No. US20030023075A1
GENERAL INFORMATION:
APPLICANT: Blatner, Frederick R.
            Burland, Valerie
            Perna, Nicole T.
            Plunkett, Guy
            Welch, Rod
TITLE OF INVENTION: No. US20030023075A1 Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1993

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      APPLICATION NUMBER: 60/110,955
      FILING DATE: 04-DEC-1998
      ATTORNEY/AGENT INFORMATION:
      NAME: Seay, Nicholas J.
      REGISTRATION NUMBER: 27386
      REFERENCE/DOCKET NUMBER: 960296.95017
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (608) 251-5000
      TELEFAX: (608) 251-9166
      INFORMATION FOR SEQ ID NO: 137:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 48908
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      MOLECULE TYPE: DNA (genomic)
      SEQUENCE DESCRIPTION: SEQ ID NO: 137:
      US-10-114-170-137

Query Match.          58.2%; Score 877.4; DB 6; Length 48908;
Best Local Similarity 99.3%; Pred. No. 1.5e-258;
Matches 881; Conservative 0; Mismatches 6; Indels 0; Gaps 0.

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Query Match	58.2%	Score 877.4	DB 6	Length 48908
Best Local Similarity	99.3%	Pred. No. 1.5e-258		
Matches 881	Conservative	0	Mismatches 6	Indels 0
			Gaps	0
QY 103	GATCTAAGGAATTTACCTTAGACCTTCTGACCTGCAAGAAAGCGATATGATTCGCTGAAT	162		
DB 30777	GTTCGGAAGAAATTACCTTAGACCTTCTGACCTGCAAGAAAGCGATATGATTCGCTGAAT	30718		
QY 163	GTCAATTCGCTCTGCAATPAGTACTCCATTACAGACTATTTTCACTAGAGGATACGCTTTA	222		
DB 30717	GTCAATTCGCTCTGCAATPAGTACTCCATTACAGACTATTTTCACTAGAGGATACGCTTTA	30658		
QY 223	CTGATGATTATATAGTGGCACAGGGGATATTTGTTTGCAGTTGATGTCAGAGGATAGAT	282		
DB 30657	CTGATGATTATATAGTGGCACAGGGGATATTTGTTTGCAGTTGATGTCAGAGGATAGAT	30598		
QY 283	CCAGAGGAAGGCGGTTTATTAATCAACGCGTTATTTGTGAAAGAAATATTTATATG	342		
DB 30597	CCAGAGGAAGGCGGTTTATTAATCAACGCGTTATTTGTGAAAGAAATATTTATATG	30538		
QY 343	ACAAGATTTGTTTAAACAGGACAAATAATGTTTTTATCGCTTTCGATTTTTCAATGTT	402		
DB 30537	ACAAGATTTGTTTAAACAGGACAAATAATGTTTTTATCGCTTTCGATTTTTCAATGTT	30478		
QY 403	ACCTTTCCAGGTACACACAGCGTTACATTTGTCTGGGACAGATACGATACACAGTTACAG	462		
DB 30477	ACCTTTCCAGGTACACACAGCGTTACATTTGTCTGGGACAGATACGATACACAGTTACAG	30418		
QY 463	CGTCTTCAGGGAATCAGTCTGACGGGATGACAGATTAATTCGCATTCGTTGACTACTTCT	522		
DB 30417	CGTCTTCAGGGAATCAGTCTGACGGGATGACAGATTAATTCGCATTCGTTGACTACTTCT	30358		
QY 523	TATCTGATTTTAATGTGCTAGTACGAACTCACTGACGAGCTGTGTGCAAGACGATG	582		
DB 30357	TATCTGATTTTAATGTGCTAGTACGAACTCACTGACGAGCTGTGTGCAAGACGATG	30298		
QY 583	TTACGAGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGCAATACAGAGGGGATTT	642		
DB 30297	TTACGAGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGCAATACAGAGGGGATTT	30238		
QY 643	CGTACACACCTGGAATGATCTCAGTGGCGGCTTTATGTATATACCTGTAAGATGTTAT	702		
DB 30237	CGTACACACCTGGAATGATCTCAGTGGCGGCTTTATGTATATACCTGTAAGATGTTAT	30178		
QY 703	CTTACATTTGACTGGGAAAGTTGAGTACGCTGCTGCTGACTATCATGACAAGACTCT	762		
DB 30177	CTTACATTTGACTGGGAAAGTTGAGTACGCTGCTGCTGACTATCATGACAAGACTCT	30118		
QY 763	GTTCGTGTAGGAAGAAATTTCTTTTGAAGCAATTAATGCAATTTCTGGAAGCGTGGCATTA	822		
DB 30117	GTTCGTGTAGGAAGAAATTTCTTTTGAAGCAATTAATGCAATTTCTGGAAGCGTGGCATTA	30058		
QY 823	ATACTGAATTTGTCAATCATGATCGCGAGTTGCCGAATGGCAATCTATAGATTTCT	882		

Db	30057	ATACGAATTGTCATCATCATGATCGCGAGTTGCCGAAATGGCATCTGATGATTTCT	29998
Qy	883	TCCTATGCTCCGGAGATGGAAGATCCGTCGGATTAACGACAAATAATATTTGGGGAT	942
Db	29997	TCCTATGCTCCGGAGATGGAAGATCCGTCGGATTAACGACAAATAATATTTGGGGAT	29938
Qy	943	TCATCCACTCTGGGGCAATTCTGATCGCGAAGACTATTAGCAGTGG	989
Db	29937	TCATCCACTCTGGGGCAATTCTGATCGCGAAGACTATTAGCAGTGG	29891
RESULT 8			
US-09-334-477-9			
Sequence 9, Application US/09334477			
Patent No. US20020012658A1			
GENERAL INFORMATION:			
APPLICANT: Williams, James A.			
Byrne, Lisa M.			
Pugh, Charles S.G.			
TITLE OF INVENTION: Prevention And Treatment Of			
Verotoxin-Induced Disease			
NUMBER OF SEQUENCES: 49			
CORRESPONDENCE ADDRES:			
ADDRESSEE: Medien & Carroll, LLP			
STREET: 220 Montgomery Street, Suite 2200			
CITY: San Francisco			
STATE: California			
COUNTRY: United States of America			
ZIP: 94104			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/334,477			
FILING DATE: 16-Jun-1999			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/816,977			
FILING DATE: <Unknown>			
ATTORNEY/AGENT INFORMATION:			
NAME: MacKnight, Kamrin T.			
REGISTRATION NUMBER: 38,230			
REFERENCE/DOCKET NUMBER: OPHD-02450			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (415) 705-8410			
TELEFAX: (415) 397-8338			
INFORMATION FOR SEQ ID NO: 9:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1241 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: double			
TOPOLOGY: linear			
MOLECULE TYPE: DNA (Genomic)			
SEQUENCE DESCRIPTION: SEQ ID NO: 9:			
US-09-334-477-9			
Query Match			
Best Local Similarity 58.2%; Score 877.2; DB 3; Length 1241;			
Matches 879; Conservative 1%; Pred. No. 1.9e-259;			
Mismatch 3; Indels 0; Gaps 0;			
Qy	108	GAAGGAATTTCCTTAGACTCTCGAGCTGGCAAAAGCATGATGTAGATTGCGTGAATGCAT	157
Db	66	GAAGGAATTTCCTTAGACTCTCGAGCTGGCAAAAGCATGATGTAGATTGCGTGAATGCAT	125
Qy	168	TCGCTCTGCAATAGGTAATCCATTACAGACTATTTCATCAGAGAGTACGCTTTACTGAT	227
Db	126	TCGCTCTGCAATAGGTAATCCATTACAGACTATTTCATCAGAGAGTACGCTTTACTGAT	185
Qy	228	CATTGATATGTCGCACAGGGGATAATTTCTTTGCGAGTTCATGCTCAGAGGATAGATCCAGA	287
Db	186	CATTGATATGTCGCCTCAGGGGATAATTTGTTTGCAAGTGTATGTCAGAGGATAGATCCAGA	245

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01 288 GGAAGGGCGGTTTAAATATCTACGGCTTATGTTGAACGAAATPATTTATATGACAG 347
02 246 GGAAGGCGGTTTAAATATCTACGGCTTATGTTGAACGAAATPATTTATATGACAG 305
03 348 ATTGTTAAACAGACAAATPATTTGTTTATCGCTTTGCTGATATTTTTCACATGTTACTT 407
04 306 ATTGTTAAACAGACAAATPATTTGTTTATCGCTTTGCTGATATTTTTCACATGTTACTT 365
05 408 TCACAGTACAAACAGGGGTTTAACTGTCTCGGTGACAGATAGCATACACAGTTACAGGGTGT 467
06 425 TCACAGGTACAAACAGGGGTTTAACTGTCTCGGTGACAGATAGCATACACAGTTACAGGGTGT 485
07 468 TGCAGGGATCAGTCGTCACGGGGATGACAGATTAATTCGCATTCGTTGACTACTTCTTAATCT 527
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13 648 AACACGTAGATGATCTCAGTGGGCGTTCTTATGATATGACTGCTGAGATGTTGATCTTAC 707
14 606 AACACGTAGATGATCTCAGTGGGCGTTCTTATGATATGACTGCTGAGATGTTGATCTTAC 665
15 708 ATTGAACCTGCGGAAAGGTTGATGAGCGTCTGCTGCTGACTATATATGACAAACCTGTTGCG 767
16 666 ATTGAACCTGCGGAAAGGTTGATGAGCGTCTGCTGCTGACTATATATGACAAACCTGTTGCG 725
17 768 TGTAGGAAGAAATTTCTTTTGAAGCAATTATATGCAATTTCTGGGAAGCGTGGCATTAATACT 827
18 726 TGTAGGAAGAAATTTCTTTTGAAGCAATTATATGCAATTTCTGGGAAGCGTGGCATTAATACT 785
19 828 GAATGTGCATTCATCATGTCATCGCGAGTTGCCAGAAATGGCATCTGATGATGTTCCCTCTAT 887
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21 888 GTGTCCGGCAGATGAAAGAGTCCGTGGGATTAACGACAAATAAATATTTGGGATTCATC 947
22 846 GTGTCCGGCAGATGAAAGAGTCCGTGGGATTAACGACAAATAAATATTTGGGATTCATC 905
23 948 CACTCTGGGGGCAATTCGATGCGGACGAACCTATTAGCAGTGG 389
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..945
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-334-477-1

Query Match 58.2%; Score 876.8; DB 3; Length 945;
Best Local Similarity 99.8%; Pred. No. 2.2e-259;
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

108 GAAGAAATTTACCTTACCTTCTGACGCAAGACGATGTGATTCGCTGATGATCAT 167
66 GAAGAAATTTACCTTACCTTCTGACGCAAGACGATGTGATTCGCTGATGATCAT 125
168 TCGCTCGCAATAGTATCTCCATTACAGACTATTTATCAGAGATACGCTTTACTGAT 227
126 TCGCTCGCAATAGTATCTCCATTACAGACTATTTATCAGAGATACGCTTTACTGAT 185
228 GATTGATAGTGGCAGAGGATATTTGTTGAGTGTGATGATGATGATGATGATGATGAT 287
186 GATTGATAGTGGCAGAGGATATTTGTTGAGTGTGATGATGATGATGATGATGATGAT 245
288 GGAAGGCGGTTTATATCTACAGGCTTATGTTGATGATGATGATGATGATGATGATGAT 347
246 GGAAGGCGGTTTATATCTACAGGCTTATGTTGATGATGATGATGATGATGATGATGAT 305
348 ATTTGTTACAGCAATATATGTTTTTATCGCTTTGCTGATTTTCACTGTTACCTT 407
306 ATTTGTTACAGCAATATATGTTTTTATCGCTTTGCTGATTTTCACTGTTACCTT 365
408 TCCAGGTACAAACGCGGTTTACATGTCGTGAGACATGATGATGATGATGATGATGATGAT 467
366 TCCAGGTACAAACGCGGTTTACATGTCGTGAGACATGATGATGATGATGATGATGATGAT 425
468 TGCAGGATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 527
426 TGCAGGATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
528 GATTTATATGTCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 587
486 GATTTATATGTCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
588 GTTTGTTACTGTGACAGCTGAAGCTTACGTTTTCGCAATATACAGAGGATTTGCTGAC 647
546 GTTTGTTACTGTGACAGCTGAAGCTTACGTTTTCGCAATATACAGAGGATTTGCTGAC 605
648 AACACTGATGATCTCAGTGGCGTTCTTATGATGATGATGATGATGATGATGATGATGAT 707
606 AACACTGATGATCTCAGTGGCGTTCTTATGATGATGATGATGATGATGATGATGATGAT 665
708 ATTAACTGGGGAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 767

Db 666 ATTGAACGTGGGGAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
Qy 768 TGTAGAAAGATTTCTTTTGGAAAGCTTATGCAATTTGGGAAGCGTGGCAATTAATCT 827
Db 726 TGTAGAAAGATTTCTTTTGGAAAGCTTATGCAATTTGGGAAGCGTGGCAATTAATCT 785
Qy 828 GAATGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 887
Db 786 GAATGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 845
Qy 888 GTGTCCGAGATGAGAGGTCGTGGGATTAAGCAATTAATTAATTTGTGGATTCATC 947
Db 846 GTGTCCGAGATGAGAGGTCGTGGGATTAAGCAATTAATTAATTTGTGGATTCATC 905
Qy 948 CACTTGGGGGCAATTCGATGCGCAGACTATTAACACT 987
Db 906 CACTTGGGGGCAATTCGATGCGCAGACTATTAACACT 945

RESULT 10

US-09-334-477-20

Sequence 20, Application US/09334477

Patent No. US20020012658A1

GENERAL INFORMATION:

APPLICANT: Williams, James A.

Byrne, Lisa M.

Pugh, Charles S. G.

TITLE OF INVENTION: Prevention And Treatment Of

Verotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/334,477

FILING DATE: 16-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/816,977

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPHD-02450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 969 base-pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..969

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-334-477-20

Query Match 58.2%; Score 876.8; DB 3; Length 969;
Best Local Similarity 99.8%; Pred. No. 2.2e-259;
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 108 GAAGGAATTTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 167
DB 66 GAAGGAATTTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 125
QY 168 TCGCTCTGCAATAGGACTCCATTCACAGACTATTTTCATCAGAGGATAGCTTTTACTGAT 227
DB 126 TCGCTCTGCAATAGGACTCCATTCACAGACTATTTTCATCAGAGGATAGCTTTTACTGAT 185
QY 228 GATTGATAGTGGCAGCAGGGGATTAATTTGTTTGCAGTTGATGTCCAGAGGATATGATCCAGA 287
DB 186 GATTGATAGTGGCAGCAGGGGATTAATTTGTTTGCAGTTGATGTCCAGAGGATATGATCCAGA 245
QY 288 GGAAGGGGGGTTTAAATCTAAGGCTTATTTGTAAGAAATATTTATATATGATACAGG 347
DB 246 GGAAGGGGGGTTTAAATCTAAGGCTTATTTGTAAGAAATATTTATATATGATACAGG 305
QY 348 ATTGTTAAACAGACAAATTAATGTTTTTATGCTTTGCTGATTTTTCACATGTTACCTT 407
DB 306 ATTGTTAAACAGACAAATTAATGTTTTTATGCTTTGCTGATTTTTCACATGTTACCTT 365
QY 408 TCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTATATACCAAGTTACAGCGTGT 467
DB 366 TCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTATATACCAAGTTACAGCGTGT 425
QY 468 TGCAGGATTCAGTGTGAGGGGATGACAGTAAATGSCCATTCGTTGACTTCTTACT 527
DB 426 TGCAGGATTCAGTGTGAGGGGATGACAGTAAATGSCCATTCGTTGACTTCTTACT 485
QY 528 GGATTTAAATGTCAGTATGAGAACTCACTGACGAGCTGTGAGCAAGAGCATGTTACG 587
DB 486 GGATTTAAATGTCAGTATGAGAACTCACTGACGAGCTGTGAGCAAGAGCATGTTACG 545
QY 588 GTTTGTTACTGTGACAGCTGAAGCTTTTACGTTTTCGCAATATACAGAGGGGATTTTCGTAC 647
DB 546 GTTTGTTACTGTGACAGCTGAAGCTTTTACGTTTTCGCAATATACAGAGGGGATTTTCGTAC 605
QY 648 AACACTGATGATATCTCAGTGGGCGTTCTTATGATATATGCTGTAAGATGTTGATCTTAC 707
DB 606 AACACTGATGATATCTCAGTGGGCGTTCTTATGATATATGCTGTAAGATGTTGATCTTAC 665
QY 708 ATTGAAGTGGGGAAGGTTGAGTAGGCTCTGCTGACTATCATGAGCAAGACTCTGTTGCG 767
DB 666 ATTGAAGTGGGGAAGGTTGAGTAGGCTCTGCTGACTATCATGAGCAAGACTCTGTTGCG 725
QY 768 TGTAGGAAGAAATTTCTTTTGAAGCATTAATGCAATTCGAGGAAACGTTGAGATTAATCT 827
DB 726 TGTAGGAAGAAATTTCTTTTGAAGCATTAATGCAATTCGAGGAAACGTTGAGATTAATCT 785
QY 828 GAATGTCATCATCATGATCGCGAGTTGCCAGAAATGCAATCTGATGATGATTTCCCTTAT 887
DB 786 GAATGTCATCATCATGATCGCGAGTTGCCAGAAATGCAATCTGATGATGATTTCCCTTAT 845
QY 888 GTGTCCGCGCAGATGGAAGAGTCCGTGGGATTAACGACATATAAATATGTTGGGATTTATC 947
DB 846 GTGTCCGCGCAGATGGAAGAGTCCGTGGGATTAACGACATATAAATATGTTGGGATTTATC 905
QY 948 CACTTGTGGGGCAATTTCTGATCCGCAAACTATTAACGCT 987
DB 906 CACTTGTGGGGCAATTTCTGATCCGCAAACTATTAACGCT 945

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RESULT 11
US-10-425-821-93
; Sequence 93, Application US/10425821
; Publication No. US20040219530A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Jos,e
; APPLICANT: BEKAL, Sadija
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/10/425,821
; CURRENT FILING DATE: 2003-04-30

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; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-425-821-93

Query Match      33.1%; Score 498.4; DB 9; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.5e-142;
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 167
DB 3 GAAGGAATTTACTTAGACTTCTGACGTCGAAGAAGCATATGATTTGGCTGATATGTCAT 62
QY 168 TCGCTCTGCAATAGGACTCCATTCACAGACTATTTTCATCAGAGGATAGCTTTTACTGAT 227
DB 63 TCGCTCTGCAATAGGACTCCATTCACAGACTATTTTCATCAGAGGATAGCTTTTACTGAT 122
QY 228 GATTGATAGTGGCAGCAGGGGATTAATTTGTTTGCAGTTGATGTCCAGAGGATATGATCCAGA 287
DB 123 GATTGATAGTGGCAGCAGGGGATTAATTTGTTTGCAGTTGATGTCCAGAGGATATGATCCAGA 182
QY 288 GGAAGGGGGGTTTAAATCTAAGGCTTATTTGTAAGAAATATTTATATATGATACAGG 347
DB 183 GGAAGGGGGGTTTAAATCTAAGGCTTATTTGTAAGAAATATTTATATATGATACAGG 242
QY 348 ATTGTTAAACAGACAAATTAATGTTTTTATGCTTTGCTGATTTTTCACATGTTACCTT 407
DB 243 ATTGTTAAACAGACAAATTAATGTTTTTATGCTTTGCTGATTTTTCACATGTTACCTT 302
QY 408 TCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTATATACCAAGTTACAGCGTGT 467
DB 303 TCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTATATACCAAGTTACAGCGTGT 362
QY 468 TGCAGGATTCAGTGTGAGGGGATGACAGTAAATGSCCATTCGTTGACTTCTTACT 527
DB 363 TGCAGGATTCAGTGTGAGGGGATGACAGTAAATGSCCATTCGTTGACTTCTTACT 422
QY 528 GGATTTAAATGTCAGTATGAGAACTCACTGACGAGCTGTGAGCAAGAGCATGTTACG 587
DB 423 GGATTTAAATGTCAGTATGAGAACTCACTGACGAGCTGTGAGCAAGAGCATGTTACG 482
QY 588 GTTTGTTACTGTGACAGCTG 607
DB 483 GTTTGTTACTGTGACAGCTG 502

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RESULT 12
US-10-765-580-10
; Sequence 10, Application US/10765580
; Publication No. US20040166565A1
; GENERAL INFORMATION:
; APPLICANT: Backer, Marina V.
; APPLICANT: Backer, Joseph M.
; TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING
; TITLE OF INVENTION: SHIGA-LIKE TOXIN AND VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 102108-300
; CURRENT APPLICATION NUMBER: US/10/765,580
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/796,861
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/190,973
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Human
US-10-765-580-10

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Query Match 33.0%; Score 498; DB 8; Length 498;
Best Local Similarity 100.0%; Pred. No. 2e-142;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGAGATCATCAGAGTGGTGAAGTTCATGATGTC 1069
DB 1 GCACCCATGCGAGAGAGAGAGAGAGAGATCATCAGAGTGGTGAAGTTCATGATGTC 60
QY 1070 TATCAGCGAGCTACTGCTCATTCATTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 1129
DB 61 TATCAGCGAGCTACTGCTCATTCATTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 120
QY 1130 GATGAGATGAGTACATCTTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 1189
DB 121 GATGAGATGAGTACATCTTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 180
QY 1190 TGCATGACGAGGAGGAGTGTGTGCTGCTGAGAGATTCACATCATCATGAGATTC 1249
DB 181 TGCATGACGAGGAGGAGTGTGTGCTGCTGAGAGATTCACATCATCATGAGATTC 240
QY 1250 ATGCGGATCAAACTTCACAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 1309
DB 241 ATGCGGATCAAACTTCACAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 300
QY 1310 AAATGTGAATGCAAGCAACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCTTGC 1369
DB 301 AAATGTGAATGCAAGCAACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCTTGC 360
QY 1370 TCAGAGCGAGAGAAAGCATTTGTTGTATCAAGATCCGAGACGTGTAAATGTTCTCGCAA 1429
DB 361 TCAGAGCGAGAGAAAGCATTTGTTGTATCAAGATCCGAGACGTGTAAATGTTCTCGCAA 420
QY 1430 AACACAGACTCGGCTTCAAGGCGAGGAGCTTGAAGTAAACGAGTACTTGCAGATGT 1489
DB 421 AACACAGACTCGGCTTCAAGGCGAGGAGCTTGAAGTAAACGAGTACTTGCAGATGT 480
QY 1490 GACAGCGGAGCGGCTGA 1507
DB 481 GACAGCGGAGCGGCTGA 498

RESULT 13

US-09-932-451A-1
; Sequence 1, Application US/09932451A
; Patent No. US2002011324A1
; GENERAL INFORMATION:
; APPLICANT: OZAMA, Keiya
; APPLICANT: SHIMPO, Masahisa
; APPLICANT: IKEDA, Yuchi
; APPLICANT: MAEDA, Yoshikazu
; APPLICANT: SHIMADA, Kazuyuki
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-MEDIATED DELIVERY OF ANGIOGENIC
; FILE REFERENCE: 0800-0026
; CURRENT APPLICATION NUMBER: US/09/932.451A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,056
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-165
; NAME/KEY: CDS
; LOCATION: (1)..(576)
US-09-932-451A-1

Query Match 33.0%; Score 498; DB 3; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.2e-142;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGATCATCAGAGTGGTGAAGTTCATGATGTC 1069
DB 79 GCACCCATGCGAGAGAGAGAGAGAGATCATCAGAGTGGTGAAGTTCATGATGTC 138
QY 1070 TATCAGCGAGCTACTGCTCATTCATTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 1129
DB 139 TATCAGCGAGCTACTGCTCATTCATTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 198
QY 1130 GATGAGATGAGTACATCTTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 1189
DB 199 GATGAGATGAGTACATCTTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 258
QY 1190 TGCATGACGAGGAGGAGTGTGTGCTGCTGAGAGATTCACATCATCATGAGATTC 1249
DB 259 TGCATGACGAGGAGGAGTGTGTGCTGCTGAGAGATTCACATCATCATGAGATTC 318
QY 1250 ATGCGGATCAAACTTCACAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 1309
DB 319 ATGCGGATCAAACTTCACAGGCGAGCATATGAGAGATGAGCTTCTTACAGCAAC 378
QY 1310 AAATGTGAATGCAAGCAACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCTTGC 1369
DB 379 AAATGTGAATGCAAGCAACCAAGAAAGATGAGCAAGCAAGAAATCCCTGTGGGCTTGC 438
QY 1370 TCAGAGCGAGAGAAAGCATTTGTTGTATCAAGATCCGAGACGTGTAAATGTTCTCGCAA 1429
DB 439 TCAGAGCGAGAGAAAGCATTTGTTGTATCAAGATCCGAGACGTGTAAATGTTCTCGCAA 498
QY 1430 AACACAGACTCGGCTTCAAGGCGAGGAGCTTGAAGTAAACGAGTACTTGCAGATGT 1489
DB 499 AACACAGACTCGGCTTCAAGGCGAGGAGCTTGAAGTAAACGAGTACTTGCAGATGT 558
QY 1490 GACAGCGGAGCGGCTGA 1507
DB 559 GACAGCGGAGCGGCTGA 576

RESULT 14

US-10-083-817-8
; Sequence 8, Application US/10083817
; Publication No. US20020193288A1
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; FILE REFERENCE: SCIOS.002C1
; CURRENT APPLICATION NUMBER: US/10/083.817
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/099,694
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 09/392,932
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-083-817-8

Query Match 33.0%; Score 498; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 2.2e-142;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGAGAGATCATCAGAGTGGTGAAGTTCATGATGTC 1069
DB 79 GCACCCATGCGAGAGAGAGAGAGAGATCATCAGAGTGGTGAAGTTCATGATGTC 138
QY 1070 TATCAGCGAGCTACTGCTCATTCATTCAGAGACCTGTGTGACATCTTCAGAGATCCCT 1129

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Db      139 TATCAGCCGAGTCTGCTCCATTCGAGACCTGTGTGACATCTTCCAGAGTACCT 198
Oy      1130 GATGAGATCGAGTACATCTTTCAGAGCCATCTGTGTGCTTGTATGCGATGCGGCGGCTGC 1189
Db      199 GATGAGATCGAGTACATCTTTCAGAGCCATCTGTGTGCTTGTATGCGATGCGGCGGCTGC 258
Oy      1190 TGCAATGACGAGGCTGTGAGTGTGTGCTTGTATGAGAGTCCATCATCATCATGAGATT 1249
Db      259 TGCAATGACGAGGCTGTGAGTGTGTGCTTGTATGAGAGTCCATCATCATCATGAGATT 318
Oy      1250 ATGCGGATCAAACTTCACCAAGCCAGCAGCATAGAGAGATGAGCTTCTTACAGACAAAC 1309
Db      319 ATGCGGATCAAACTTCACCAAGCCAGCAGCATAGAGAGATGAGCTTCTTACAGACAAAC 378
Oy      1310 AAATGTGAATGACAGCAAAAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369
Db      379 AAATGTGAATGACAGCAAAAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438
Oy      1370 TCAGAGCGGAGAAAGCAATTTGTTGTACAGATCCGAGAGCTGTAAATGTTCTGCAAA 1429
Db      439 TCAGAGCGGAGAAAGCAATTTGTTGTACAGATCCGAGAGCTGTAAATGTTCTGCAAA 498
Oy      1430 AACACAGACTCGCTTGCAGAGCGAGAGCTTGAAGTTAAAGAGCTACTTGCAGATGT 1489
Db      499 AACACAGACTCGCTTGCAGAGCGAGAGCTTGAAGTTAAAGAGCTACTTGCAGATGT 558
Oy      1490 GACAAAGCCGAGCGGTGA 1507
Db      559 GACAAAGCCGAGCGGTGA 576

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RESULT 15
US-10-268-447-5
; Sequence 5, Application US/10268447
; Publication No. US20030096754A1
; GENERAL INFORMATION:
; APPLICANT: N. Stephen Pollitt
; APPLICANT: Judith A. Abraham
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
; TITLE OF INVENTION: VARIANTS
; FILE REFERENCE: SCIOS.004DV1
; CURRENT APPLICATION NUMBER: US/10/268,447
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/135,312
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/574,708
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(573)
US-10-268-447-5

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Query Match      33.0%; Score 498; DB 6; Length 576;
Best Local Similarity 100.0%; Pred. No. 2,2e-142;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      1010 GACCCATGCGAGAGAGAGAGAGAGAGAGATCATCAGAGAGTGTGAAGTTTCATGATGTC 1069
Db      79 GACCCATGCGAGAGAGAGAGAGAGAGAGATCATCAGAGAGTGTGAAGTTTCATGATGTC 138
Oy      1070 TATCAGCGGAGTACTGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1129
Db      139 TATCAGCGGAGTACTGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 198
Oy      1130 GATGAGATCGAGTACATCTTTCAGAGCCATCTGTGTGCTTGTATGAGAGTGCAGAGTACCT 1189
Db      199 GATGAGATCGAGTACATCTTTCAGAGCCATCTGTGTGCTTGTATGAGAGTGCAGAGTACCT 258

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Oy      1190 TGCAATGACGAGGCTGTGAGTGTGTGCTTGTATGAGAGTCCATCATCATCATGAGATT 1249
Db      259 TGCAATGACGAGGCTGTGAGTGTGTGCTTGTATGAGAGTCCATCATCATCATGAGATT 318
Oy      1250 ATGCGGATCAAACTTCACCAAGCCAGCAGCATAGAGAGATGAGCTTCTTACAGACAAAC 1309
Db      319 ATGCGGATCAAACTTCACCAAGCCAGCAGCATAGAGAGATGAGCTTCTTACAGACAAAC 378
Oy      1310 AAATGTGAATGACAGCAAAAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1369
Db      379 AAATGTGAATGACAGCAAAAGAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438
Oy      1370 TCAGAGCGGAGAAAGCAATTTGTTGTACAGATCCGAGAGCTGTAAATGTTCTGCAAA 1429
Db      439 TCAGAGCGGAGAAAGCAATTTGTTGTACAGATCCGAGAGCTGTAAATGTTCTGCAAA 498
Oy      1430 AACACAGACTCGCTTGCAGAGCGAGAGCTTGAAGTTAAAGAGCTACTTGCAGATGT 1489
Db      499 AACACAGACTCGCTTGCAGAGCGAGAGCTTGAAGTTAAAGAGCTACTTGCAGATGT 558
Oy      1490 GACAAAGCCGAGCGGTGA 1507
Db      559 GACAAAGCCGAGCGGTGA 576

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Job time : 2111 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:26:15 ; Search time 313 Seconds

(without alignments)

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Title: US-10-765-580-11

Perfect score: 1507

Sequence: 1 atgacacatcatcatcatca.....gtgacaaagcgagcggtga 1507

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93555401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents NA:*

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- 2: /EMC_Celerra_SIDS3/prodata/2/ina/5 COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	881.4	58.5	2073	US-08-816-977-46	Sequence 46, Appl
2	881.4	58.5	2073	US-09-334-477-46	Sequence 46, Appl
3	879.4	58.4	2127	US-08-816-977-32	Sequence 32, Appl
4	879.4	58.4	2127	US-09-334-477-32	Sequence 32, Appl
5	878.4	58.3	981	US-08-816-977-36	Sequence 36, Appl
6	878.4	58.3	981	US-09-334-477-36	Sequence 36, Appl
7	877.4	58.2	48908	US-09-453-7028-137	Sequence 137, App
8	877.4	58.2	48908	US-10-114-170-137	Sequence 137, App
9	877.2	58.2	1241	US-08-816-977-9	Sequence 9, Appl
10	877.2	58.2	1241	US-09-334-477-9	Sequence 9, Appl
11	876.8	58.2	945	US-08-816-977-1	Sequence 1, Appl
12	876.8	58.2	945	US-09-334-477-1	Sequence 1, Appl
13	876.8	58.2	969	US-08-816-977-20	Sequence 20, Appl
14	876.8	58.2	969	US-09-334-477-20	Sequence 20, Appl
15	505.8	33.6	1299	PCT-US95-10973A-58	Sequence 58, Appl
16	502.4	33.3	1809	PCT-US95-10973A-79	Sequence 79, Appl
17	498	33.0	576	US-09-392-932-8	Sequence 8, Appl
18	498	33.0	576	US-09-574-708A-5	Sequence 5, Appl
19	498	33.0	576	US-09-392-931-5	Sequence 5, Appl
20	498	33.0	576	US-10-266-447-5	Sequence 5, Appl
21	498	33.0	576	US-10-418-529-5	Sequence 5, Appl
22	498	33.0	605	US-08-718-904-2	Sequence 2, Appl
23	498	33.0	605	US-09-449-249-2	Sequence 2, Appl

24	498	33.0	605	7	PCT-US95-10973A-26	Sequence 26, Appl
25	498	33.0	649	3	US-09-949-016-1168	Sequence 1168, Ap
26	498	33.0	989	10	5332671-11	Patent No. 5332671
27	498	33.0	990	3	US-08-567-200A-1	Sequence 1, Appl
28	498	33.0	990	3	US-08-591-794-1	Sequence 1, Appl
29	498	33.0	990	3	US-08-882-816-1	Sequence 1, Appl
30	498	33.0	990	3	US-08-802-052B-1	Sequence 1, Appl
31	498	33.0	990	4	US-07-795-006A-1	Sequence 1, Appl
32	498	33.0	990	4	US-09-880-107-2336	Sequence 2336, Ap
33	498	33.0	990	5	US-09-346-069-1	Sequence 1, Appl
34	498	33.0	2136	3	US-09-587-184-1	Sequence 1, Appl
35	498	33.0	3583	3	US-09-976-594-921	Sequence 921, App
36	498	33.0	5163	3	US-09-919-039-166	Sequence 166, App
37	498	33.0	5610	3	US-09-655-493B-2	Sequence 2, Appl
38	496.4	32.9	498	10	5194586-20	Patent No. 5194586
39	496.4	32.9	498	10	5219739-21	Patent No. 5219739
40	496.4	32.9	990	3	US-08-734-443-13	Sequence 13, Appl
41	495.2	32.9	1269	7	PCT-US95-10973A-32	Sequence 32, Appl
42	495	32.8	599	7	PCT-US95-10973A-89	Sequence 89, Appl
43	493.4	32.7	1369	7	PCT-US95-10973A-33	Sequence 33, Appl
44	489	32.4	599	7	PCT-US95-10973A-87	Sequence 87, Appl
45	447.6	29.7	961	10	5219739-16	Patent No. 5219739

ALIGNMENTS

RESULT 1
US-08-816-977-46
Sequence 46, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816, 977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 2073 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2070
US-08-816-977-46

Query Match 58.5%; Score 881.4; DB 3; Length 2073;
 Best Local Similarity 99.3%; Pred. No. 3.7e-273;
 Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 99 CCCAGATCGAAGGATTTACTTCTGACCTTCGCACTGCAAGAGCTATGTAGATTCGCT 158
DB 1182 CCCGGAATTCAGGAATTTACTTCTGACCTTCGCACTGCAAGAGCTATGTAGATTCGCT 1241
QY 159 GAATGTCATTCGCTTCGCAATAGTATCTCATTAAGACTATTTTCATGAGAGTACGTC 218
DB 1242 GAATGTCATTCGCTTCGCAATAGTATCTCATTAAGACTATTTTCATGAGAGTACGTC 1301
QY 219 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
DB 1302 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1361
QY 279 AGATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 338
DB 1362 AGATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1421
QY 339 TGTGACAGGATTTGTTACAGCAAAATATGTTTTTATCGCTTTCGATTTTTCACA 398
DB 1422 TGTGACAGGATTTGTTACAGCAAAATATGTTTTTATCGCTTTCGATTTTTCACA 1481
QY 399 TGTTCATCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGATGACATGATACAGCT 458
DB 1482 TGTTCATCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGATGACATGATACAGCT 1541
QY 459 ACAGCGTGTTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
DB 1542 ACAGCGTGTTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1601
QY 519 TTTCTATCTGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 578
DB 1602 TTTCTATCTGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1661
QY 579 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
DB 1662 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1721
QY 639 ATTTGCTGACAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
DB 1722 ATTTGCTGACAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1781
QY 699 TGAATCTTACATTAATCTGAGGAAAGTTGAGTACGCTGCTGCTGATCATGACAAACA 758
DB 1782 TGAATCTTACATTAATCTGAGGAAAGTTGAGTACGCTGCTGCTGATCATGACAAACA 1841
QY 759 CTCTGTTGCTGTAAGAAATTTCTTTTGGAGCAATTAATGCAATTCGAGGAGGCTGAC 818
DB 1842 CTCTGTTGCTGTAAGAAATTTCTTTTGGAGCAATTAATGCAATTCGAGGAGGCTGAC 1901
QY 819 ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
DB 1902 ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1961
QY 879 TCTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
DB 1962 TCTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2021
QY 939 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
DB 2022 GATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2072
  
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RESULT 2
 US-09-334-477-46
 ; Sequence 46, Application US/09334477
 ; Patent No. 6652857
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, James A.
 ; Byrne, Lisa M.

Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of
 Verotoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/334,477

FILING DATE: 16-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/816,977

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPND-02450

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 2073 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2070

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-334-477-46

Query Match

Best Local Similarity 99.3%; Score 881.4; DB 3; Length 2073;

Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 99 CCCAGATCGAAGGATTTACTTCTGACCTTCGCACTGCAAGAGCTATGTAGATTCGCT 158
DB 1182 CCCGGAATTCAGGAATTTACTTCTGACCTTCGCACTGCAAGAGCTATGTAGATTCGCT 1241
QY 159 GAATGTCATTCGCTTCGCAATAGTATCTCATTAAGACTATTTTCATGAGAGTACGTC 218
DB 1242 GAATGTCATTCGCTTCGCAATAGTATCTCATTAAGACTATTTTCATGAGAGTACGTC 1301
QY 219 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
DB 1302 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1361
QY 279 AGATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 338
DB 1362 AGATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1421
QY 339 TGTGACAGGATTTGTTACAGCAAAATATGTTTTTATCGCTTTCGATTTTTCACA 398
DB 1422 TGTGACAGGATTTGTTACAGCAAAATATGTTTTTATCGCTTTCGATTTTTCACA 1481
QY 399 TGTTCATCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGATGACATGATACAGCT 458
DB 1482 TGTTCATCTTTCCAGGTACAAACAGCGGTTTCAATTGCTGTGATGACATGATACAGCT 1541
QY 459 ACAGCGTGTTCAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 518
  
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Db      1542  ACACGGTGTGACAGGATCATGCTGTACGGAGATGCAATAAATGCGATTCGTTGACTAC
Qy      519   TTCTTATCTGGATTAAATGTCAGTACAGTACCTCAGTACAGTCTGTGSCAGAGC
Db      1602  TTCTTATCTGGATTAAATGTCAGTACAGTACCTCAGTACAGTCTGTGSCAGAGC
Qy      579   GATGTACGGTTTGTATCTGTACAGTCAAGCTTAACTGTTTGGCAATACAGAGGG
Db      1662  GATGTACGGTTTGTATCTGTACAGTCAAGCTTAACTGTTTGGCAATACAGAGGG
Qy      639   ATTTCGACAACTGTATGATCTCAGTGGGCGTTTATGATATGATCTGCTGAAGATG
Db      1722  ATTTCGACAACTGTATGATCTCAGTGGGCGTTTATGATATGATCTGCTGAAGATG
Qy      699   TGATCTTACATTGAATGAGGAGGAGTTGATAGAGCTCTGCTATCATGAGCAAGA
Db      1782  TGATCTTACATTGAATGAGGAGGAGTTGATAGAGCTCTGCTATCATGAGCAAGA
Qy      759   CTCTGTTCGTGTAGAGAGATTTCTTTTGGAGCATTAATGCAATTTCTGGAGCGTGGC
Db      1842  CTCTGTTCGTGTAGAGAGATTTCTTTTGGAGCATTAATGCAATTTCTGGAGCGTGGC
Qy      819   ATTAATCTGAATGTGATCATCATCATGAGGAGTCCAGATGCGCAATGCGCATCTGATG
Db      1902  ATTAATCTGAATGTGATCATCATCATGAGGAGTCCAGATGCGCAATGCGCATCTGATG
Qy      879   TCCTTCTATGTGTCGGCAGATGAGAGATCCGTGGATTACGACAAATTAATTTGTG
Db      1962  TCCTTCTATGTGTCGGCAGATGAGAGATCCGTGGATTACGACAAATTAATTTGTG
Qy      939   GGATTCATCCACTCTGGGGGCAATTTCTGATGCGGAGACTATTTAGCAGTGG
Db      2022  GGATTCATCCACTCTGGGGGCAATTTCTGATGCGGAGACTATTTAGCAGTGG

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RESULT 3

US-08-816-977-32

Sequence 32, Application US/08816977

Patent No. 6080400

GENERAL INFORMATION:

APPLICANT: Williams, James A.

APPLICANT: Byrne, Lisa M.

APPLICANT: Pugh, Charles S.G.

TITLE OF INVENTION: Prevention And Treatment Of

TITLE OF INVENTION: Verofoxin-Induced Disease

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/816,977

FILING DATE: 13-MAR-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPND-02450

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 2127 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2127
; US-08-816-977-32

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Query Match 58.4%; Score 879.4; DB 3; Length 2127;

Best Local Similarity 99.3%; Pred. No. 1.7e-272;

Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      101   CAGATCTGAAGAATTTACTCTAGACTTCTGCACTGCAAGAAGTATGATGCTGCTGA
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Qy      161   ATGTCAATTCGCTCTGCAATAGTACTCTCATTAAGATATTTTATCATGAGAGTACGCTTT
Db      1298  ATGTCAATTCGCTCTGCAATAGTACTCTCATTAAGATATTTTATCATGAGAGTACGCTTT
Qy      221   TACTGATGATGATGATGTCGACAGGGGATTAATTTGTTGCACTTGAATGTCAGAGGATAG
Db      1358  TACTGATGATGATGATGTCGCTCAGGGGATTAATTTGTTGCACTTGAATGTCAGAGGATAG
Qy      281   ATCCAGAGAGAGGCGGCTTTAATTAATCTACGGCTTAATGTTGTAAGCAATTAATTTATAG
Db      1418  ATCCAGAGAGAGGCGGCTTTAATTAATCTACGGCTTAATGTTGTAAGCAATTAATTTATAG
Qy      341   TGACAGATTTGTTAAGAGACAAATATGTTTTATGCTTGTGATTTTTCATAG
Db      1478  TGACAGATTTGTTAAGAGACAAATATGTTTTATGCTTGTGATTTTTCATAG
Qy      401   TTACTCTTCCAGGTACAAACAGCGGTTACATTTCTGTGTGACACTACTATACACAGCTTAC
Db      1538  TTACTCTTCCAGGTACAAACAGCGGTTACATTTCTGTGTGACACTACTATACACAGCTTAC
Qy      461   AGCGGTGTCAGGAGATCAAGTCTGACGGGATGAGATTAATCCGCAATTCCTGACTACTT
Db      1598  AGCGGTGTCAGGAGATCAAGTCTGACGGGATGAGATTAATCCGCAATTCCTGACTACTT
Qy      521   CTATATCGATTTAATGTGTCATAGTGAACCTCACTGACGCAAGTCTGTGCAAGAGCGA
Db      1658  CTATATCGATTTAATGTGTCATAGTGAACCTCACTGACGCAAGTCTGTGCAAGAGCGA
Qy      581   TGTTCAGGTTGTTTACGTGTACAGCTGACCTTACCTTTCCGCAATACAGAGGGGAT
Db      1718  TGTTCAGGTTGTTTACGTGTACAGCTGACCTTACCTTTCCGCAATACAGAGGGGAT
Qy      641   TTGGTACAAACATGATGATCTCAGTGGGCGTTCTTATGTAATGACTGTGAAGATGTTG
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Qy      701   ATCTTACATTGAATCTGGGAGAGTTGATAGGCTCTGCTGCTGATCATGACACACT
Db      1838  ATCTTACATTGAATCTGGGAGAGTTGATAGGCTCTGCTGCTGATCATGACACACT
Qy      761   CTGTTCGTGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAGAGCGTGGCAT
Db      1898  CTGTTCGTGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAGAGCGTGGCAT
Qy      821   TAATACGAAATGTGATCATCATGATCGGAGTTGCGAATGTCAGATGAGTTTC
Db      1958  TAATACGAAATGTGATCATCATGATCGGAGTTGCGAATGTCAGATGAGTTTC
Qy      881   CTCTATGTGTCCGCGAGATGAGAGTCCGTGGGATTTAGCGCAATTAATATTTGGG
Db      2018  CTCTATGTGTCCGCGAGATGAGAGTCCGTGGGATTTAGCGCAATTAATATTTGGG
Qy      941   ATTATCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG
Db      2078  ATTATCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG

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RESULT 4
US-09-334-477-32
Sequence 32, Application US/09334477
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPND-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 2127 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2127
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-334-477-32
Query Match 58.4%; Score 879.4; DB 3; Length 2127;
Best Local Similarity 99.3%; Pred. No. 1.7e-212;
Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 101 CAGATCGAAGAAATTACCTAGACTCTGCACTGCAAGACGATGATGATTCGCTGA 160
DB 1238 CAGAAATTCAGAAATTTACTTACCTTACCTTCCGACGTGAAGAGCTATGATTCGCTGA 1297
QY 161 ATGTCTTGGCTCTGCAATAGGTAATTCATTCATTAACAGACTATTTTCAACGAGGTAAGCTCTT 220
DB 1298 ATGTCTTGGCTCTGCAATAGGTAATTCATTCATTAACAGACTATTTTCAACGAGGTAAGCTCTT 1357
QY 221 TACTGATGATTAATGAGCAACAGGGGATTAATTTGTTGAGTTGATGAGGAGTAG 280
DB 1358 TACTGATGATTAATGAGCAACAGGGGATTAATTTGTTGAGTTGATGAGGAGTAG 1417
QY 281 ATCCAGAGGAAGGCGGCTTAATATCTACGCGCTTATTTGAAAGAAATTAATTAATG 340
DB 1418 ATCCAGAGGAAGGCGGCTTAATATCTACGCGCTTATTTGAAAGAAATTAATTAATG 1477
QY 341 TGACAGATTTGTTAAAGCAAAATATATGTTTTTATCGCTTGCTGATTTTTCACATG 400

DB 1478 TGACAGATTTGTTAAAGCAAAATATATGTTTTTATCGCTTGCTGATTTTTCACATG 1537
QY 401 TTACTCTTCAGGTAACAACAGGGTTACATTTGTCGGTGAACAGTAGATATACCAAGTTAC 460
DB 1538 TTACTCTTCAGGTAACAACAGGGTTACATTTGTCGGTGAACAGTAGATATACCAAGTTAC 1597
QY 461 AGCGTTGTCAGGATCAGTGTGACGCGGATGACAGATTAATTCGCCATTGTTGACTACTT 520
DB 1598 AGCGTTGTCAGGATCAGTGTGACGCGGATGACAGATTAATTCGCCATTGTTGACTACTT 1657
QY 521 CTATTCGATTAATTAATGTCGATAGTGAACCTCACTACGCAAGTCTTGCCAGAGGGA 580
DB 1658 CTATTCGATTAATTAATGTCGATAGTGAACCTCACTACGCAAGTCTTGCCAGAGGGA 1717
QY 581 TGTTACGGTTGTTGATCTGTAAGCTGAAGCTTTATGTTTGGCAATTAACAGAGGAT 640
DB 1718 TGTTACGGTTGTTGATCTGTAAGCTGAAGCTTTATGTTTGGCAATTAACAGAGGAT 1777
QY 641 TTCCGTAACAACCTGATGATCTGAGTGGCGCTTCTTAATGTAATGACTGTAAGATGTTG 700
DB 1778 TTCCGTAACAACCTGATGATCTGAGTGGCGCTTCTTAATGTAATGACTGTAAGATGTTG 1837
QY 701 ATCTTAATGTAATCTGGGGAAGTTGAGTAGCGTCTGCTGACTATATGATGACAAGACT 760
DB 1838 ATCTTAATGTAATCTGGGGAAGTTGAGTAGCGTCTGCTGACTATATGATGACAAGACT 1897
QY 761 CTGTCGATGTAAGGAATTTCTTTTGGAGCAATTAATGCAATTCGGAAGCGTGCAAT 820
DB 1898 CTGTCGATGTAAGGAATTTCTTTTGGAGCAATTAATGCAATTCGGAAGCGTGCAAT 1957
QY 821 TAATCTGAATTTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 880
DB 1958 TAATCTGAATTTGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2017
QY 881 CTTCATATGTCGCGCAATGGAAGATCCGCGGATTAATGCAATTAATTAATTTGTTG 940
DB 2018 CTTCATATGTCGCGCAATGGAAGATCCGCGGATTAATGCAATTAATTAATTTGTTG 2077
QY 941 ATTCATCCACTCTGGGGCAATTCGATGCGGAGCAATTAATTAATTAATTTGTTG 989
DB 2078 ATTCATCCACTCTGGGGCAATTCGATGCGGAGCAATTAATTAATTAATTTGTTG 2126

RESULT 5
US-08-816-977-36
Sequence 36, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Macknight, Kamrin T.
REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..981
US-08-816-977-36

Query Match 58.3%; Score 878.4; DB 3; Length 981;
Best Local Similarity 97.2%; Pred. No. 2.1e-272;
Matches 894; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

70 GCTAATTCGACCGCAGACATGACAGCCAGATCGAAGAACTTACCTTAGACTTC 129
61 GCTGACTCAAGAGAGAGATGACAGAGCTTGAATTCAGAACTTACCTTAGACTTC 120
130 TCGACTGCAAGAGAGATGATGCTGGAATGCTGCTGCAATAGTACTGCA 189
121 TCGACTGCAAGAGAGATGATGCTGGAATGCTGCTGCAATAGTACTGCA 180
190 TTACAGACTATTTTCAGAGAGATGCTGCTTACTGATGATGATGAGCAAGGGAT 249
181 TTACAGACTATTTTCAGAGAGATGCTGCTTACTGATGATGATGAGCAAGGGAT 240
250 AATTGTTTGCAGTGTAGTCAAGAGGATATCCAGAGAGAGGGGCTTAAATATCTA 309
241 AATTGTTTGCAGTGTAGTCAAGAGGATATCCAGAGAGAGGGGCTTAAATATCTA 300
310 CGGCTTATTTGTTGAAGAAATATTTATATGTCAGAGATTTGTTAAGAGCAAAATAT 369
301 CGGCTTATTTGTTGAAGAAATATTTATATGTCAGAGATTTGTTAAGAGCAAAATAT 360
370 GTTTTATTCGCTTGTGATTTTTCACATGTTACCTTTCAGAGTACCAAGCGTTACA 429
361 GTTTTATTCGCTTGTGATTTTTCACATGTTACCTTTCAGAGTACCAAGCGTTACA 420
430 TTGTCGTGAGCAGTATGATACAGAGTTCAGAGGATGAGTGTAGTACAGGGG 489
421 TTGTCGTGAGCAGTATGATACAGAGTTCAGAGGATGAGTGTAGTACAGGGG 480
490 ATGCAGATTAATCGCATTCGTTGACTACTTCTTATCTGATTTAATGTCGATAGTGA 549
481 ATGCAGATTAATCGCATTCGTTGACTACTTCTTATCTGATTTAATGTCGATAGTGA 540
550 ACCCTACTGAGCAGTCTGTGCAAGAGGATGTTACGGTTTGTACTGTGACAGCTGAA 609
541 ACCCTACTGAGCAGTCTGTGCAAGAGGATGTTACGGTTTGTACTGTGACAGCTGAA 600
610 GCTTACGTTTTCGCAATACAGAGGGGATTTGTAACAACCTGAGATTCAGTGG 669
601 GCTTACGTTTTCGCAATACAGAGGGGATTTGTAACAACCTGAGATTCAGTGG 660
670 GCTTCTTATGTAATGACTGCTGAGATGTTGATCTTCACTTGAACCTGGGAAAGTTGAGT 729
661 GCTTCTTATGTAATGACTGCTGAGATGTTGATCTTCACTTGAACCTGGGAAAGTTGAGT 720
730 AGCGTCTGCTGATCATATGACAGAGCTCTGTTCTGTATGAGAAAGATTTCTTTTGA 789
721 AGCGTCTGCTGATCATATGACAGAGCTCTGTTCTGTATGAGAAAGATTTCTTTTGA 780
790 AGCATTAATGCAATCTGGGAGCGTGGCAATTAATGCAATTTGTCATCATCATCATCAG 849
781 AGCATTAATGCAATCTGGGAGCGTGGCAATTAATGCAATTTGTCATCATCATCATCAG 840
850 CGAGTTGCGAGAAATGCAATCTGATGAGTTTCTTCTATGTTGTCGCGAGATGGAAGATC 909

841 CGAGTTGCGAGAAATGCAATCTGATGAGTTTCTTCTATGTTGTCGCGAGATGGAAGATC 900
910 CGTGGATTAAGCAATTAATTTGTGGATTAATCCACTCTGGGGGCAATTCATG 969
901 CGTGGATTAAGCAATTAATTTGTGGATTAATCCACTCTGGGGGCAATTCATG 960
970 CGCAGAACTATTACAGTGG 989
961 CGCAGAACTATTACAGTGG 980

RESULT 6
US-09-334-477-36
Sequence 36.6652857
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Karlin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..981
SEQUENCE DESCRIPTION: SEQ ID NO: 36;
US-09-334-477-36

Query Match 58.3%; Score 878.4; DB 3; Length 981;
Best Local Similarity 97.2%; Pred. No. 2.1e-272;
Matches 894; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

70 GCTAATTCGACCGCAGACATGACAGCCAGATCGAAGAACTTACCTTAGACTTC 129
61 GCTGACTCAAGAGAGAGATGACAGAGCTTGAATTCAGAACTTACCTTAGACTTC 120
130 TCGACTGCAAGAGAGATGATGCTGGAATGCTGCTGCAATAGTACTGCA 189
121 TCGACTGCAAGAGAGATGATGCTGGAATGCTGCTGCAATAGTACTGCA 180

Oy	190	TTTACAGACTAATTTCAACAGAGAGTACGCTTTTACGATGATTTGATATGGCAACAGGGAT	249
Ds	181	TTTACAGACTAATTTCAACAGAGAGTACGCTTTTACGATGATTTGATATGGCTCAGGGAT	240
Oy	250	AATTTGTTTGCAGTTGATGTCCAGAGGATAGATCCAGAGGAGGCGGTTTAATCTA	309
Ds	241	AATTTGTTTGCAGTTGATGTCCAGAGGATAGATCCAGAGGAGGCGGTTTAATCTA	300
Oy	310	CGGCTTATTTGTGAACGAATAATTTATATGTGACAGAGATTTTGTAAACAGACAAATAT	359
Ds	301	CGGCTTATTTGTGAACGAATAATTTATATGTGACAGAGATTTTGTAAACAGACAAATAT	350
Oy	370	GTTTTTATATGCTTGTCTGATTTTTCACATGTACCTTCCAGGTCACACAGCGTTACA	429
Ds	361	GTTTTTATATGCTTGTCTGATTTTTCACATGTACCTTCCAGGTCACACAGCGTTACA	420
Oy	430	TTGTCTGTGACAGTAGACTATACACGTTACAGCGTGTGACAGGATCAGTCCAGCGGG	489
Ds	421	TTGTCTGTGACAGTAGACTATACACGTTACAGCGTGTGACAGGATCAGTCCAGCGGG	480
Oy	490	ATGCAGATTAATGCGCATTCGTTGTGACTCTTATCTTGATTTTAATGTCGATATGGGA	549
Ds	481	ATGCAGATTAATGCGCATTCGTTGTGACTCTTATCTTGATTTTAATGTCGATATGGGA	540
Oy	550	ACCTCACTGACGAGCTGTGGCAAGAGGATGTATACGTTGTTTACTGTGACAGCTGAA	609
Ds	541	ACCTCACTGACGAGCTGTGGCAAGAGGATGTATACGTTGTTTACTGTGACAGCTGAA	600
Oy	610	GCTTTACGTTTTCCGCAAAATACAGAGGGATTTGCTACAACACTGATGATCTCAGTGGG	669
Ds	601	GCTTTACGTTTTCCGCAAAATACAGAGGGATTTGCTACAACACTGATGATCTCAGTGGG	660
Oy	670	CGTTCTTATATATGACTGCTGAAGTGTGATCTTACATTTGAACCTGGGAAAGGTTAGT	729
Ds	661	CGTTCTTATATATGACTGCTGAAGTGTGATCTTACATTTGAACCTGGGAAAGGTTAGT	720
Oy	730	AGGCTCTGCTGACTATCATGACACAAGCTCTGTTGCTGATAGAAAGATTTCTTTTGA	789
Ds	721	AGGCTCTGCTGACTATCATGACACAAGCTCTGTTGCTGATAGAAAGATTTCTTTTGA	780
Oy	790	AGCATTAATGCAATTTCTGGGAAAGCTGGGCAATTAAATCTGAATATGTCATCATCATGCAATCG	849
Ds	781	AGCATTAATGCAATTTCTGGGAAAGCTGGGCAATTAAATCTGAATATGTCATCATCATGCAATCG	840
Oy	850	CGAGTTCCGAAATGGGATCTGATGAGTTTCCCTCTATATGTCGCGGACGATGAGAAAGTC	909
Ds	841	CGAGTTCCGAAATGGGATCTGATGAGTTTCCCTCTATATGTCGCGGACGATGAGAAAGTC	900
Oy	910	CGTGGGATTAACGACAATAAATATTTGTGGATTCATCCACTCTGGGGCAATTTCTGATG	965
Ds	901	CGTGGGATTAACGACAATAAATATTTGTGGGATTCATCCACTCTGGGGCAATTTCTGATG	960
Oy	970	CGCAGAACTATATGACATCG	989
Ds	961	CGCAGAACTATATGACATCG	980

RESULT 7
US-09-453-702B-137/C
; Sequence 137, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blatner, Frederick

TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street

CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296, 95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9126
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 48908
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 137:
US-09-453-702B-137

Query Match	98.2%:	Score 877.4:	DB 3:	Length 48908:
Best Local Similarity	59.3%:	Pred. No. 5.5e-271:		
Matches 881:	Conservative 0:	Mismatches 6:	Indels 0:	Gaps 0:
QY	103	GATCTGAAGAAATTTACCTTAGACCTTCTGCAGTCAAGACGTAATGTAGATTGCGTGAAT	162	
Db	30777	GTTCGCGAAGAAATTTACCTTAGACCTTCTGCAGTCAAGACGTAATGTAGATTGCGTGAAT	30718	
QY	163	GTCATTGCGCTTCGCATATAGTACTCTCCATTACAGACTATTTCAATCGAGAGTACGCTTTA	222	
Db	30717	GTCATTGCGCTTCGCATATAGTACTCTCCATTACAGACTATTTCAATCGAGAGTACGCTTTA	30658	
QY	223	CTGTGATGTATGATGTGSCACAGGGGATTAATTTGGTTGACGTTGATGTCAGAGGGATAGAT	282	
Db	30657	CTGTATGATGTATGATGTGSCACAGGGGATTAATTTGGTTGACGTTGATGTCAGAGGGATAGAT	30598	
QY	283	CCAGAGAGAGGGCGGTTTAAATAATCTACGGCTTATGTTGAAAGAAATATTTATATGTG	342	
Db	30597	CCAGAGAGAGGGCGGTTTAAATAATCTACGGCTTATGTTGAAAGAAATATTTATATGTG	30538	
QY	343	ACAGGATTTGTTAACAGAGCAATAATGTTTTTATCGCTTTCGTAATTTTTCACATGTT	402	
Db	30537	ACAGGATTTGTTAACAGAGCAATAATGTTTTTATCGCTTTCGTAATTTTTCACATGTT	30478	
QY	403	ACCTTTCAGAGTCAACAGCGGTTACATTGTCGAGCAGATAGCTATACCAAGTTACG	462	
Db	30477	ACCTTTCAGAGTCAACAGCGGTTACATTGTCGAGCAGATAGCTATACCAAGTTACG	30418	
QY	463	CGTGTTCAGAGGATCACTCGTACGGGGATGCAGATAATGCGCATTTGTTGACTACTTCT	522	
Db	30417	CGTGTTCAGAGGATCACTCGTACGGGGATGCAGATAATGCGCATTTGTTGACTACTTCT	30355	
QY	523	TATCTGATTTAATGTGCGATATCTGGAACCTCACAGCAGCTGTGCGAAGAGCGATG	582	
Db	30357	TATCTGATTTAATGTGCGATATCTGGAACCTCACAGCAGCTGTGCGAAGAGCGATG	30295	
QY	583	TTACGATTGTTACTGTCGACAGCTGAAGCTTTACGTTTTCGCGCAATATCAGAGGGGATTT	642	
Db	30297	TTACGATTGTTACTGTCGACAGCTGAAGCTTTACGTTTTCGCGCAATATCAGAGGGGATTT	30238	

QY 643 CGTACAACTGATGATCTGAGTGGGCTTATATGATGATGATGATGAT 702
DB 30237 CGTACAACTGATGATCTGAGTGGGCTTATATGATGATGATGAT 30178
QY 703 CTTACATGAACTGAGGAGGTTGAGTGGGCTTATATGATGATGATGAT 762
DB 30177 CTTACATGAACTGAGGAGGTTGAGTGGGCTTATATGATGATGATGAT 30118
QY 763 GTTGTGTAGAGAGATTTCTTTTGAAGCATTAATGCAATTCGGGAAGCGTGCATTA 822
DB 30117 GTTGTGTAGAGAGATTTCTTTTGAAGCATTAATGCAATTCGGGAAGCGTGCATTA 30058
QY 823 ATACGATTTGATCATCATGATGATGATGATGATGATGATGATGATGAT 882
DB 30057 ATACGATTTGATCATCATGATGATGATGATGATGATGATGATGATGAT 29998
QY 883 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGGGAT 942
DB 29997 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGGGAT 29938
QY 943 TCATCCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 989
DB 29937 TCATCCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 29891

RESULT 8
US-10-114-170-137/c
Sequence 137, Application US/10114170
Patent No. 6855814

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.

Perna, Nicole T.

Melich, Rod

TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSER: Charles & Brady

STREET: 1 South Plinkney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM: Medium type: Diskette, 3.50 inch, 1.44mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,170

FILING DATE: 01-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/453,702

FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296, 95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 137:

LENGTH: 48908

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 137:

US-10-114-170-137

Query Match

Best Local Similarity 99.3%; Score 877.4; DB 3; Length 48908;

Best Local Similarity 99.3%; Pred. No. 5,56-271;

Matches 881; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 103 GATCTGAGGAGATTTACCTTACGATCTTCTGACATGCAAGAGATGATGATGAT 162
DB 30777 GTTGTGTAGAGAGATTTACCTTACGATCTTCTGACATGCAAGAGATGATGATGAT 30718
QY 163 GTATTCGCTCTGCAATAGGATCTCATTAAGATTAATTTATCATGAGGATGAT 222
DB 30717 GTATTCGCTCTGCAATAGGATCTCATTAAGATTAATTTATCATGAGGATGAT 30658
QY 223 CTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
DB 30657 CTGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 30598
QY 283 CCAGAGAGAGGCGGTTTAATTAATCTACGCTTATTTGTAACGAAATTAATTAATG 342
DB 30597 CCAGAGAGAGGCGGTTTAATTAATCTACGCTTATTTGTAACGAAATTAATTAATG 30538
QY 343 ACAGATTTTGTAAACAGACAAATTAATGTTTATGCTTGTGATTTTCAATG 402
DB 30537 ACAGATTTTGTAAACAGACAAATTAATGTTTATGCTTGTGATTTTCAATG 30478
QY 403 ACCTTTCCAGGTAAACAGCGGTTTACATTTGCTGATGATGATGATGATGATGAT 462
DB 30477 ACCTTTCCAGGTAAACAGCGGTTTACATTTGCTGATGATGATGATGATGATGAT 30418
QY 463 CGTGTTCAGGAGATCACTGTCAGCGGATGATGATGATGATGATGATGATGATGAT 522
DB 30417 CGTGTTCAGGAGATCACTGTCAGCGGATGATGATGATGATGATGATGATGATGAT 30358
QY 523 TATCTGATTTTAATGTCGATATGGAACCTCACTGACGATCTGTCGCAAGCGATG 582
DB 30357 TATCTGATTTTAATGTCGATATGGAACCTCACTGACGATCTGTCGCAAGCGATG 30298
QY 583 TTACGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 642
DB 30297 TTACGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 30238
QY 643 CGTACAACTGATGATCTGAGTGGGCTTATATGATGATGATGATGATGAT 702
DB 30237 CGTACAACTGATGATCTGAGTGGGCTTATATGATGATGATGATGATGAT 30178
QY 703 CTTACATGAACTGAGGAGGTTGAGTGGGCTTATATGATGATGATGATGAT 762
DB 30177 CTTACATGAACTGAGGAGGTTGAGTGGGCTTATATGATGATGATGATGAT 30118
QY 763 GTTGTGTAGAGAGATTTCTTTTGAAGCATTAATGCAATTCGGGAAGCGTGCATTA 822
DB 30117 GTTGTGTAGAGAGATTTCTTTTGAAGCATTAATGCAATTCGGGAAGCGTGCATTA 30058
QY 823 ATACGATTTGATCATCATGATGATGATGATGATGATGATGATGATGATGAT 882
DB 30057 ATACGATTTGATCATCATGATGATGATGATGATGATGATGATGATGATGAT 29998
QY 883 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGGGAT 942
DB 29997 TCTATGTCTCCGCGAGATGAGAGAGTCCGTGGGATTAAGCAATTAATTAATTTGGGAT 29938
QY 943 TCATCCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 989
DB 29937 TCATCCACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTTG 29891

RESULT 9

US-08-816-977-9

Sequence 9, Application US/08816977

Patent No. 6080400

GENERAL INFORMATION:

APPLICANT: Williams, James A.

APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1241 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-816-977-9

Query Match 58.2%; Score 877.2; DB 3; Length 1241;
Best Local Similarity 99.7%; Pred. No. 6,1e-272;
Matches 879; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACCTTAGACTTCTGACTGCAAAAGCGTATGATGCTGCTGATGCTAT 167
DB 66 GAAGGAATTTACCTTAGACTTCTGACTGCAAAAGCGTATGATGCTGCTGATGCTAT 125
QY 168 TCCGCTGCAATAGTATCTCCATTCAGACTATTTTCAGAGGATACGCTTACTGAT 227
DB 126 TCCGCTGCAATAGTATCTCCATTCAGACTATTTTCAGAGGATACGCTTACTGAT 185.
QY 228 GATTGATAGTGCAGACAGGATATTTGTTGCGATGATGTCAGAGGATAGATCCAGA 287
DB 186 GATTGATAGTGCAGACAGGATATTTGTTGCGATGATGTCAGAGGATAGATGAGAGA 245
QY 288 GGAAGCGCGTTTATATATCTAGCGCTTATTTGAAAGAAATATTTATATGTCAGAG 347
DB 246 GGAAGCGCGTTTATATATCTAGCGCTTATTTGAAAGAAATATTTATATGTCAGAG 305
QY 348 ATTGTTACAGAGCAATATATGTTTTTATCGCTTGCATTTTACATGTTACTT 407
DB 306 ATTGTTACAGAGCAATATATGTTTTTATCGCTTGCATTTTACATGTTACTT 365
QY 408 TCCAGTACAAACAGCGTTACATTTGCTGTGTCAGATAGCTATACACAGCGTGT 467
DB 366 TCCAGTACAAACAGCGTTACATTTGCTGTGTCAGATAGCTATACACAGCGTGT 425
QY 468 TGCAGGATCAGTGTACGGGATGCGATTAATCCGCAATTCCTTCTTATCT 527
DB 426 TGCAGGATCAGTGTACGGGATGCGATTAATCCGCAATTCCTTCTTATCT 485
QY 528 GGATTTATATGTCGATAGTGAAGCTCAGTACGACGCTGTGTGGCAGAGGATGTTACG 587
DB 486 GGATTTATATGTCGATAGTGAAGCTCAGTACGACGCTGTGTGTGGCAGAGGATGTTACG 545

QY 588 GTTTGTTACTGTGACAGCTGAAAGCTTTACGTTTTCGGCAAAATACAGAGGATTTCTGAC 647
DB 546 GTTTGTTACTGTGACAGCTGAAAGCTTTTACGTTTTCGGCAAAATACAGAGGATTTCTGAC 605
QY 648 AACACTGATGATCTCAGTGGCGCTTTCTTATGTAATGACTGCTGAAAGTGTGATCTTAC 707
DB 606 AACACTGATGATCTCAGTGGCGCTTTCTTATGTAATGACTGCTGAAAGTGTGATCTTAC 665
QY 708 ATTGAACGGGGAGGCTTGAGAGCGTCGCTGACTATCATGGAACAAGACTGTTG 767
DB 666 ATTGAACGGGGAGGCTTGAGAGCGTCGCTGACTATCATGGAACAAGACTGTTG 725
QY 768 TGTAGAGAAATTTCTTTGGAAGCATTAATGCAATTTGCGAAGCGTGGCATTAATCT 827
DB 726 TGTAGAGAAATTTCTTTGGAAGCATTAATGCAATTTGCGAAGCGTGGCATTAATCT 785
QY 828 GAATTTGATCATCATGATGATGCGGATGTCGCAAGATGCGATGATGATGTTCTTCTAT 887
DB 786 GAATTTGATCATCATGATGATGCGGATGTCGCAAGATGCGATGATGATGATGTTCTTCTAT 845
QY 888 GTGTCGGGAGATGGAAGAGTCGCGGATTTACGCAATTAATTTGTGGATTTCAATC 947
DB 846 GTGTCGGGAGATGGAAGAGTCGCGGATTTACGCAATTAATTTGTGGATTTCAATC 905
QY 948 CACTCTGGGGCAATTTGATGTCGCGAAGATTAATTTAGCAGTGG 989
DB 906 CACTCTGGGGCAATTTGATGTCGCGAAGATTAATTTAGCAGTGG 947

RESULT 10
US-09-334-477-9
Sequence 9, Application US/09334477
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1241 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-334-477-9

Query Match 58.2%; Score 877.2; DB 3; Length 1241;
Best Local Similarity 99.7%; Pred. No. 6,1e-272;
Matches 879; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 108 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATATGCGGATGTCAT 167
DB 66 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATATGCGGATGTCAT 125
QY 168 TCGCTTCGCAATAGTACTCCATTACAGACTATTTTCATCAGAGGTAAGTCTTTACTGAT 227
DB 126 TCGCTTCGCAATAGTACTCCATTACAGACTATTTTCATCAGAGGTAAGTCTTTACTGAT 185
QY 228 GATTGATAGTGGCAGAGGGATTAATTTGTTGCGAGTTGATGTGACAGGATATCCAGA 287
DB 186 GATTGATAGTGGCAGAGGGATTAATTTGTTGCGAGTTGATGTGACAGGATATCCAGA 245
QY 288 GGAAGGGCGGTTTAAATATCTAAGGCTTATGTTGAACGAATAATTTATATGAGACAG 347
DB 246 GGAAGGGCGGTTTAAATATCTAAGGCTTATGTTGAACGAATAATTTATATGAGACAG 305
QY 348 ATTGTTAACAGACAAATAATGTTTTTATCGCTTGTGATTTTTCACATGTTACTCT 407
DB 306 ATTGTTAACAGACAAATAATGTTTTTATCGCTTGTGATTTTTCACATGTTACTCT 365
QY 408 TCCAGGTACAAACAGCGGTTACATGTTCTGTGAGACATGCTATACACGTTACAGCGTGT 467
DB 366 TCCAGGTACAAACAGCGGTTACATGTTCTGTGAGACATGCTATACACGTTACAGCGTGT 425
QY 468 TGCAGGGATCAGTGTGACGGGGATGACATTAATGCGCATTCGTTACTTCTTACT 527
DB 426 TGCAGGGATCAGTGTGACGGGGATGACATTAATGCGCATTCGTTACTTCTTACT 485
QY 528 GGATTTTAAATGTCGATAGTGAACCTCACTGACGAGCTGTGCGAAGAGCGATGTTACG 587
DB 486 GGATTTTAAATGTCGATAGTGAACCTCACTGACGAGCTGTGCGAAGAGCGATGTTACG 545
QY 588 GTTGTGTTACTGTGACAGCTGAAGCTTTTACGTTTTCGGAATAACAGAGGGATTTCTGAC 647
DB 546 GTTGTGTTACTGTGACAGCTGAAGCTTTTACGTTTTCGGAATAACAGAGGGATTTCTGAC 605
QY 648 AACACTGATGATCTCACTGAGGCGTTCTTATGTAATGCTGCTGAAGATGTTGATCTTAC 707
DB 606 AACACTGATGATCTCACTGAGGCGTTCTTATGTAATGCTGCTGAAGATGTTGATCTTAC 665
QY 708 ATTGAACCTGGGAAAGTTGAGTACGCTCTGCTGATCATGACACAAAGCTCTGTTCCG 767
DB 666 ATTGAACCTGGGAAAGTTGAGTACGCTCTGCTGATCATGACACAAAGCTCTGTTCCG 725
QY 768 TGTGAGGAAGATTTCTTTGAGACATTAATGCAATTTGCGAAGCGGTGATTAATGCT 827
DB 726 TGTGAGGAAGATTTCTTTGAGACATTAATGCAATTTGCGAAGCGGTGATTAATGCT 785
QY 828 GAATTTGATCATGATCATGATCGCAGATGCGCAGATGSCATCTGATGATTTCTTCTGAT 887
DB 786 GAATTTGATCATGATCATGATCGCAGATGCGCAGATGSCATCTGATGATTTCTTCTGAT 845
QY 888 GTGTCCGCGACAGATGAGAGTCCGTGGATTTACGACAAATAATTTGTTGGGATTCATC 947
DB 846 GTGTCCGCGACAGATGAGAGTCCGTGGATTTACGACAAATAATTTGTTGGGATTCATC 905
QY 948 CACTCTGGGGGCAATTTCTGATGCGAGAACTATTAAGCAGTGG 989
DB 906 CACTCTGGGGGCAATTTCTGATGCGAGAACTATTAAGCAGTGG 947
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RESULT 11
US-08-816-977-1
; Sequence 1, Application US/08816977
; Patent No. 6080400
; GENERAL INFORMATION:

```
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPBD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..945
US-08-816-977-1
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Query Match 58.2%; Score 876.8; DB 3; Length 945;
Best Local Similarity 99.8%; Pred. No. 6,8e-272;
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 108 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATATGCGGATGTCAT 167
DB 66 GAAGGAATTTACCTTACCTTCTGACGCGAAGACGATATGCGGATGTCAT 125
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RESULT 13
US-08-816-977-20
Sequence 20, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPND-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 969 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..969
US-08-816-977-20
Query Match 58.2%; Score 876.8; DB 3; Length 969;
Best Local Similarity 99.8%; Pred. No. 6.9e-272;
Matches 878; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 108 GAAGAAATTTACCTTAGACTTCTGACGCAAGACGATGATGCTGCTGAATGTCAT 167
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QY 168 TCGCTCTGCATAGTACTTCCATTCACACTATTTTCATCAGAGAGTACTTCTTACTAT 227
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RESULT 14
US-09-334-477-20
Sequence 20, Application US/09334477
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230

GenCore version 5.1.9
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Title: US-10-765-580-11

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Gap 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: gb_ba: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	881.4	58.5	2073	AR099894	AR099894 Sequence
2	881.4	58.5	2073	AR431428	AR431428 Sequence
3	880.4	58.4	1238	AB015056	AB015056 Escherich
4	880.4	58.4	1369	E27911	E27911 Method for
5	880.4	58.4	1601	AF461168	AF461168 Escherich
6	880.4	58.4	6921	EC0413275	AJ413275 Bacteriop
7	880.4	58.4	7333	AY638795	AY638795 Stx1-conv
8	880.4	58.4	57930	LPH556162	AJ556162 Phage BP-
9	879.6	58.4	6014	SPY271153	AJ271153 Shigella
10	879.4	58.4	2127	AR099884	AR099884 Sequence
11	879.4	58.4	2127	AR431418	AR431418 Sequence
12	879	58.3	1238	AB030485	AB030485 Escherich
13	879	58.3	1362	SSO132761	AJ132761 Shigella
14	879	58.3	1500	SHFSMT	M19437 S.dysenter
15	879	58.3	1956	AF461172	AJ461172 Escherich
16	879	58.3	8053	SSO279086	AJ279086 Shigella
17	879	58.3	32094	AF15317	AF15317 Shigella
18	879	58.3	110000	CP000034_12	Continuation (13 o

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ALIGNMENTS

RESULT 1	AR099894	2073 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR099894	Sequence	46 from patent US 6080400.		
DEFINITION	AR099894				
ACCESSION	AR099894.1	GI:12810342			
KEYWORDS	AR099894.1				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2073)				
AUTHORS	Williams,J.A. and Byrne,L.Marie.				
TITLE	Compositions for the prevention and treatment of verotoxin-induced disease				
JOURNAL	Patent: US 6080400-A 46 27-JUN-2000;				
FEATURES	Location/Qualifiers				
source	1..2073				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				

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QY	159	GAATGTCATTCGCTTCGCAATAGTACTTCATTACAGACTATTTTCATCAGAGTACGTC	218	
DB	1242	GAATGTCATTCGCTTCGCAATAGTACTTCATTACAGACTATTTTCATCAGAGTACGTC	1301	
QY	219	TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	278	
DB	1302	TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1361	
QY	279	AGATCAGAGGAGGCGGTTTAATATCTACGCGCTTATGTTGAACGAAATTAATTATA	338	
DB	1362	AGATCAGAGGAGGCGGTTTAATATCTACGCGCTTATGTTGAACGAAATTAATTATA	1421	

QY	339	TGTGACAGATTTTGTGTTAAACAGAACAAATTAAGTTTTTTATTCGCTTTCGATATTTTTCACA	398		
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QY	399	TGTTAACCTTTCCAGGTACACAGACGGTGTACATTGTCTGTGACAGTAGTATTAACCAAGCTT	458		
DB	1482	TGTTAACCTTTCCAGGTACACAGACGGTGTACATTGTCTGTGACAGTAGTATTAACCAAGCTT	1541		
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DB	1542	ACAGCGTGTCCAGGGATCAGTCCGTACGGGGATCCAGATTAATCCGATTCGTTGACTAC	1601		
QY	519	TTCTTATCTGATTTAATATGTGCAATAGTGAACCTCACTGACGCAAGTCTGTGGCAAGC	578		
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QY	579	GATGTACCGGTTTGTGTACTGTGACACTGGAAGCTTTACGTTTGGCAATACAGAGGG	638		
DB	1662	GATGTACCGGTTTGTGTACTGTGACACTGGAAGCTTTACGTTTGGCAATACAGAGGG	1721		
QY	639	ATTTCGTACCAACACGTGATGTATCTCAGTGGGCGTTCTTATATGATATGACTGTGAAATGT	698		
DB	1722	ATTTCGTACCAACACGTGATGTATCTCAGTGGGCGTTCTTATATGATATGACTGTGAAATGT	1781		
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LOCUS	AR431428	2073 bp	DNA linear PAT 18-DEC-2003		
DEFINITION	Sequence 46 from patent US 6652857.				
ACCESSION	AR431428				
VERSION	AR431428.1	GI:40193464			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2073)				
AUTHORS	Williams,J.A., Byrne,L.M. and Pugh,C.S.G.				
TITLE	Methods for producing avian venorexin antitoxin				
JOURNAL	Patent: US 6652857-A 46 25-NOV-2003;				
FEATURES	Promega Corporation; Madison, WI				
source	Location/Qualifiers				
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Query Match	58.5%; Score 881.4; DB 2; Length 2073;				
Best Local Similarity	99.3%; Pred. No. 2.1e-252;				
Matches	885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY	99	CCGAGATCTGAAGAATTTACTTTCAGCTTCTCGACTGCAAGACGTATGTAGATTGCT	158		
DB	1182	CCCGAATTCAAGGAATTTTACTTTCAGCTTCTCGACTGCAAGACGTATGTAGATTGCT	1241		

Oy	159	GAATGATTCGCTCGCAATAGGATCTCATTTACAGATATTTATCATGAGAGGATACGC	218
Db	1242	GAATGATTCGCTCGCAATAGGATCTCATTTACAGATATTTATCATGAGAGGATACGC	1301
Oy	219	TTTACTGATGATGATGATAGTGCGCACAGGGGATATATTTGTTGACAGTTGATGTCAGAGGAT	278
Db	1302	TTTACTGATGATGATGATAGTGCGCACAGGGGATATATTTGTTGACAGTTGATGTCAGAGGAT	1361
Oy	279	AGATCCAGAGAGAGGGCGGTTTATATATCTACAGGCTTATTTGTGAACGAATATATTAT	338
Db	1362	AGATCCAGAGAGAGGGCGGTTTATATATCTACAGGCTTATTTGTGAACGAATATATTAT	1421
Oy	339	TGAGACAGGATTTGTTTACAGGACCAATATGTTTTTATCGCTTGCGATTTTTCACA	398
Db	1422	TGAGACAGGATTTGTTTACAGGACCAATATGTTTTTATCGCTTGCGATTTTTCACA	1481
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Oy	459	ACAGCGTTTGCAAGGATCAGTGTACCGGGATATGCAATTAATCCGATTCGTTGACTAC	518
Db	1542	ACAGCGTTTGCAAGGATCAGTGTACCGGGATATGCAATTAATCCGATTCGTTGACTAC	1601
Oy	519	TTCTTATCTGGAATTTATATGTCGATATGTGGAACTTACTAGACGCACTCTGTGGCAAGAC	578
Db	1602	TTCTTATCTGGAATTTATATGTCGATATGTGGAACTTACTAGACGCACTCTGTGGCAAGAC	1661
Oy	579	GATGTTCACGGTTGTTTACTGTGACAGCTGAAGCTTTACGTTTTCGGCCAATATACAGAGGG	638
Db	1662	GATGTTCACGGTTGTTTACTGTGACAGCTGAAGCTTTACGTTTTCGGCCAATATACAGAGGG	1721
Oy	639	ATTTCGTACCAACTGTGATATCTCAGTGGCGCTTATATGATATACATGCTGAAGATG	698
Db	1722	ATTTCGTACCAACTGTGATATCTCAGTGGCGCTTATATGATATACATGCTGAAGATG	1781
Oy	699	TGATCTTACATTTGAACCTGCGGAAGTTGAATAGCTACGCTCCCTGACTATCATGAGACAGA	758
Db	1782	TGATCTTACATTTGAACCTGCGGAAGTTGAATAGCTACGCTCCCTGACTATCATGAGACAGA	1841
Oy	759	CTCTGTTCGTGTAGGAAGAAATTTCTTTTGAAGCATTAATGCAAAATTCGTGGAAAGCGGTGC	818
Db	1842	CTCTGTTCGTGTAGGAAGAAATTTCTTTTGAAGCATTAATGCAAAATTCGTGGAAAGCGGTGC	1901
Oy	819	ATTAAATCTGAATTTGATCATCATGATGCGAGGTTGCAGAAATGGCATCTGATGAGTT	878
Db	1902	ATTAAATCTGAATTTGATCATCATGATGCGAGGTTGCAGAAATGGCATCTGATGAGTT	1961
Oy	879	TCCCTTATATGATGTCGCGACAGATGGAAGATCCGTGGGATTACGCACAAATTAATTTGTG	938
Db	1962	TCCCTTATATGATGTCGCGACAGATGGAAGATCCGTGGGATTACGCACAAATTAATTTGTG	2021
Oy	939	GGATTTCATCCACTCTGGGGGCAATTTCTGATGCCGACAACTATTATGCACTGTG	989
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RESULT 3			
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LOCUS			
DEFINITION		Escherichia coli genes for shiga-like toxin 1 A-subunit, shiga-like	
ACCESSION		ABO15056.1 GI:6527100	
KEYWORDS		shiga-like toxin 1 B-subunit; scx1 A-subunit; shiga-like toxin 1	
SOURCE		A-subunit; scx1 A-subunit.	
ORGANISM		Escherichia coli	
REFERENCE		Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
AUTHORS		Enterobacteriaceae; Escherichia.	
		1 (sites), Makino, S., Maekura, H., Kobori, H. and Morimoto, Y.	

TITLE
Detection of *Escherichia coli* O157:H7 from *Musca domestica* (Diptera: Muscidae) at a cattle farm in Japan

JOURNAL
J. Med. Entomol. 36 (1), 108-112 (1999)

PUBMED
10071501

REFERENCE
2 (bases 1 to 1238)

AUTHORS
Makino, S.

TITLE
Submitted

JOURNAL
Direct Submission

Submitted (28-MAY-1998) Sou-ichi Makino, Obihiro University of Agriculture and Veterinary Medicine, Department of Veterinary Microbiology; Inada-cho, Obihiro, Hokkaido 080-8555, Japan (E-mail: smakino@obihiro.ac.jp, Tel: 81-155-49-5386, Fax: 81-155-49-5402)

FEATURES
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Query Match 58.4%; Score 880.4; DB 15; Length 1238;
Best Local Similarity 99.9%; Pred. No. 4,4e-252;
Matches 881; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 GAAGGAATTTAGCTTCTGACGCAAGAAGCGATGTGAGTTCGCTGAATGTCAT 167
DB 66 GAAGGAATTTAGCTTCTGACGCAAGAAGCGATGTGAGTTCGCTGAATGTCAT 125
QY 168 TCGCTCTGCAATAGTACTCCATTACAGACTATTTTCATCAGAGGAGTACTTTACTGAT 227
DB 126 TCGCTCTGCAATAGTACTCCATTACAGACTATTTTCATCAGAGGAGTACTTTACTGAT 185
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QY 468 TGCAGGATCAGTCGTACGGGGGATGCGAATAATCCCATTCGTTGACTACTTCTATCT 527
DB 426 TGCAGGATCAGTCGTACGGGGGATGCGAATAATCCCATTCGTTGACTACTTCTATCT 485
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RESULT 4
LOCUS E27911 1369 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for detecting foreign DNA fragment insert in Vero toxin gene.
ACCESSION E27911
VERSION E27911.1 GI:13020764
KEYWORDS JP 1999243996-A/1.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
REFERENCE 1 (bases 1 to 1369)
AUTHORS Masahiro, K., Yoshiaki, N., Yoshinisa, K. and Kunihiko, S.
TITLE Method for detecting foreign DNA fragment insert in Vero toxin gene
JOURNAL Patent: JP 1999243996-A 1 14-SEP-1999;
TOYOBO CO LTD
OS Escherichia coli
PN JP 1999243996-A/1
PD 14-SEP-1999
PF 27-FEB-1998 JP 1998047677
PI MASAHIRO KUSUMOTO, YOSHIKI NISHIYA, YOSHINISA KAMAMURA, PI
KUNIHICO SHINAGAWA
PC C1201/68, C12N15/09/// (C12N15/09, C12R1:185), C12N15/00, (C12N15/00, PC C12R1:185)
CC Topology: Linear;
FH key Location/Qualifiers
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FT /organism="Escherichia coli".
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ORIGIN /db_xref="taxon:562"

Query Match 58.4%; Score 880.4; DB 2; Length 1369;
Best Local Similarity 99.9%; Pred. No. 4.4e-252;
Matches 881; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACCTTGTAGCTTCGACCTGCAAGAGCTGTGATGATGCTGCAATGCTAT 167
DB 98 GAAGGAATTTACCTTGTAGCTTCGACCTGCAAGAGCTGTGATGATGCTGCAATGCTAT 157
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QY 888 GTGTCCGCGAGATGGAAGAGTCCGTGGGATTTAGCGACAAATTAATTTGGGATTCATC 947
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QY 948 CACTCTGGGGGCAATTCGATGGCGACAACTATTAGAGTGG 989
DB 938 CACTCTGGGGGCAATTCGATGGCGACAACTATTAGAGTGG 979

RESULT 5
AF461168 1601 bp DNA linear BCT 01-JUN-2002
LOCUS Escherichia coli EK201 Shiga toxin 1A subunit (stx1A) and Shiga
DEFINITION toxin 1B subunit (stx1B) genes, complete cds.

ACCESSION AF461168
VERSION AF461168.1 GI:21636520
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1 (bases 1 to 1601)
Yu, J.Y., Jeon, H.G., Kang, Y.H., Kim, B.C., Sohn, C.K. and Lee, B.K.
Characterization of Shiga toxin genes in Shiga toxin-producing
Escherichia coli isolated in Korea
Unpublished
2 (bases 1 to 1601)
Yu, J.Y., Jeon, H.G., Kang, Y.H., Kim, B.C., Sohn, C.K. and Lee, B.K.
Direct Submission
Submitted (19-DEC-2001) Dept. of Microbiology, National Institute
of Health, Korea, 5 Nohbon-dong Eumyong-gu, Seoul 122-701, Korea
Location/Qualifiers
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ORIGIN

Query Match 58.4%; Score 880.4; DB 15; Length 1601;
Best Local Similarity 99.9%; Pred. No. 4.3e-252;
Matches 881; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACCTTGTAGCTTCGACCTGCAAGAGCTGTGATGATGCTGCAATGCTAT 167
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QY 168 TCGCTTCGCAATAGTACTCTCAATTAACAATAATTCATCAGAGGATGCTTTACTAT 227
DB 158 TCGCTTCGCAATAGTACTCTCAATTAACAATAATTCATCAGAGGATGCTTTACTAT 217
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DB 218 GATTGATAGTGACACAGGGGATATTTGTTGAGTATGTCAGAGGATATGATCCAGA 277
QY 288 GGAAGGGCGGTTTAATATCTAGCGCTTAATGTTGATGAGCAATATTAATATGATCAGG 347
DB 278 GGAAGGGCGGTTTAATATCTAGCGCTTAATGTTGATGAGCAATATTAATATGATCAGG 337

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Oy	468	TGCAGGGATTCAGTGGTACGGGGATGACATATAATCCGATTCGTTGACTCTTATCT	527
Oy	718	TGCAGGGATTCAGTGGTACGGGGATGACATATAATCCGATTCGTTGACTCTTATCT	777
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Oy	778	GGATTTAATGTCGCATATGTCGAACCTCACTGACAGCGAGTCTGTGGCAAGAGCGATGTTACG	837
Oy	588	GTTTGTTAAGTGTGACAGCTTAAAGCTTTACGTTTTCGGCAATATACAGAGGGATTTTCGAT	647
Oy	838	GTTTGTTAAGTGTGACAGCTTAAAGCTTTACGTTTTCGGCAATATACAGAGGGATTTTCGAT	897
Oy	648	AACACTGATGATCTCAGTGGGCGCTTCTATATGTAATGATCTGTAAGATGTTGATCTTAC	707
Oy	898	AACACTGATGATCTCAGTGGGCGCTTCTATATGTAATGATCTGTAAGATGTTGATCTTAC	957
Oy	708	ATTGAACGTGGGGAAGGTTGAGTAGAGCGTCTGTGCTGACTATCATGTGACAAAGCTCTGTTGG	767
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Oy	828	GAATTTGTCATCATCATGATGCGAGCGAGTTCGCCAGATGGCATCTGATGAGTTCCTCTAT	887
Oy	1078	GAATTTGTCATCATCATGATGCGAGCGAGTTCGCCAGATGGCATCTGATGAGTTCCTCTAT	1137
Oy	888	GTCGTCGGGCAATGGGAAGATGTCCTGGGATTAACGCAATATAATTTGTGGGATTCATC	947
Oy	1138	GTCGTCGGGCAATGGGAAGATGTCCTGGGATTAACGCAATATAATTTGTGGGATTCATC	1197
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RESULT 6			
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LOCUS			
DEFINITION	Bacteriophage Lahn1 proviral nina gene (partial), ORF92, ORF71, ORF78, ninf gene, ORF175, ninf gene, ORF13, ORF350, ORF51, roi gene, ninf gene, ninf gene, q gene, stx1a gene and stx1b gene (partial).		
ACCESSION	AJ413275		
VERSION	AJ413275.1	GI:23343476	
KEYWORDS	late anti-terminator; nina gene; ninf gene; ninf gene; ninf gene; ninf gene; ORF13; ORF175; ninf gene; ORF350; ORF51; ORF71; ORF78; ORF92; q gene; recombination endonuclease; roi gene; Roi protein; shiga toxin 1, subunit A; shiga toxin 1, subunit B; stx1a gene; stx1b gene.		
SOURCE	Bacteriophage Lahn1		
ORGANISM	Bacteriophage Lahn1		
REFERENCE	1		
AUTHORS	El-Sayed, A.A.A.		
TITLE	Molecular characterisation of two shiga toxin encoding bacteriophages from enterohaemorrhagic Escherichia coli		
JOURNAL	Thesis (2000) Department of Veterinary Medicine, Justus-Liebig-University, D-35392 Giessen, Germany		
REFERENCE	2		
AUTHORS	El-Sayed, A.A.A., Wieler, L.H., Baljer, G., Stamm, I. and Kroeger, M.		
TITLE	Identification of Shiga toxin producing prophages in E.coli from bovine reveal new insights into toxic phage evolution		
JOURNAL	Unpublished		

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REFERENCE      3 (bases 1 to 6921)
AUTHOR        Kroeger M.
TITLE         Direct Submision
JOURNAL       Submitted (24-SEP-2001) Kroeger M., Inst. f. Mikrobiology and
              Molecularbiol., Justus-Liebig-University, Heinrich-Buff-Ring 26-32,
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Query Match	Best Local Similarity	58.4%	Score 880.4	DB 3	Length 6921
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				Gaps	0
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DB 5770	GAGGAATTTACCTTAGACTCTTCGACTGCAAGAACGCTAATGTAATTCGCTGAATGCAT	5822			
QY 168	TCGCTCGCAATAGGATACCTCCATTAAGACTATTTTCATCAGAGGATACGCTCTTACTGAT	227			
DB 5830	TCGCTCGCAATAGGATACCTCCATTAAGACTATTTTCATCAGAGGATACGCTCTTACTGAT	5885			
QY 228	GATTGATAGTGGACAGAGGGATTAATTTGTTGCACTGATGTCAGAGGATAGATCCAGA	287			
DB 5890	GATTGATAGTGGACAGAGGGATTAATTTGTTGCACTGATGTCAGAGGATAGATCCAGA	5944			
QY 288	GGAAGGCGGTTTAATTAATCTACAGGCTTAATTTGTTGCACTGATGTCAGAGGATAGATCCAGA	347			
DB 5950	GGAAGGCGGTTTAATTAATCTACAGGCTTAATTTGTTGCACTGATGTCAGAGGATAGATCCAGA	6005			
QY 348	ATTGTTTAACAGGCAATATATGTTTAAATCGCTTGCATGATTTTTCATATGTTACCTT	407			
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QY 408	TCCAGTACAAACAGCGGTTACATTTGTCGTGAGACAGTAGACTAATCAACGTTACAGCGTGT	467			
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QY 468	TGCAGGATCACTGCTACGGGATGACAGATTAATCCGCAATTCGTTGACTACTCTTATCT	527			
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QY 528	GGATTTAATGTCGATAGTGGAACTCACTACGACAGCTGTGCGCAAGAGCGATGTTACG	587			
DB 6190	GGATTTAATGTCGATAGTGGAACTCACTACGACAGCTGTGCGCAAGAGCGATGTTACG	6244			
QY 588	GTTTGTACTGTGCAACCTGAAGCTTTACGTTTTCGCAAAATACAGAGGGGATTTTCGTCAC	647			
DB 6250	GTTTGTACTGTGCAACCTGAAGCTTTACGTTTTCGCAAAATACAGAGGGGATTTTCGTCAC	6303			
QY 648	AACACTGATATCTCACTGAGGCGTTCTTAATGTAATGATCTGCAAGATGTTGATCTTAC	707			
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Db	1472	GGATTTAAATGTCGATAGTGAACCTCACTGACGAGTCTGTGGAGAGCGATGTTACG	1531
Qy	588	GTTTGTACTCTGACAGCTGAAGCTTTTACGTTTTGGCAAAAACAGAGGGGATTCGTAC	647
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DEFINITION	Phage BP-4795 complete genome.		
ACCESSION	AJ556162	AY487680	
VERSION	AJ556162.1	GI:49523585	
KEYWORDS	antiterminal protein Ant; antitermination protein N; ant gene; antirepressor protein Q; avirulence protein; bet gene; Bet protein; ci gene; cii gene; ciii gene; complete genome; cro gene; dam gene; damage-inducible protein DinI; dinI gene; DNA N-6-adenine-methyltransferase Dam; DNA-binding protein Roi; endopeptidase Rz; excisionase; exo gene; exonuclease; gam gene; head-tail adaptor; host-nuclease inhibitor protein Gam; hypothetical protein; hypothetical protein Yhs; int gene; integrase; kil gene; Kil protein; large subunit terminase; lom gene; major head protein/prohead protease; major tail subunit; minor tail protein; N gene; nih gene; Nihb protein; nung gene; Ning protein; nihg gene; Nihp protein; O gene; outer membrane protein Lm precursor; P gene; pep3 gene; portal protein; O gene; R gene; R protein; regulatory protein CII; regulatory protein CIII; regulatory protein Cro; ren gene; Ren protein; replication protein O; replication protein P; repressor protein Ci; roi gene; Rz gene; S gene; S protein; Shiga toxin 1 subunit A; Shiga toxin 1 subunit B; single-stranded DNA binding protein; stxai gene; stxai gene; tail assembly chaperone; tail component; tail fiber component; tail fiber protein; transposase OrfA protein of 15629; transposase OrfB protein of 15629; type III secretion system effector; xis gene;		
SOURCE	Yhs gene.		
ORGANISM	Phage BP-4795		
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae; Lambda-like viruses; unclassified Lambda-like viruses.		
AUTHORS	Creutzburg, K., Recktenwald, J., Kuhle, V., Herold, S., Hensel, M. and		

TITLE	Schmidt H.
JOURNAL	The Shiga Toxin 1-Converting Bacteriophage BP-4795 Encodes an
PUBMED	NleA-like Type III Effector Protein
REFERENCES	J. Bacteriol. 187 (24), 8494-8498 (2005)
AUTHORS	16321954
TITLE	2 (bases 1 to 57930)
JOURNAL	Schmidt H.
REFERENCE	Direct Submission
AUTHORS	Submitted (12-APR-2003) Schmidt H., Institute of Medical
TITLE	Microbiology and Hy, Technical University of Dresden,
JOURNAL	Pectinesterase 74, D-01307 Dresden, GERMANY
REMARK	revised by [3]
COMMENT	3 (bases 1 to 57930)
FEATURES	Schmidt H.
SOURCE	Direct Submission
	Submitted (06-JUL-2005) Schmidt H., Department of Food
	Microbiology, Institute of Food Technology, University of
	Hohenheim, Garbenstrasse 28, D-70599 Stuttgart, GERMANY
	On Aug 3, 2005 this sequence version replaced gi:10910914.
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QY	168	TCGCTCTGCATAATAGTATCTCCATTTACAGACTATTTTATCATCAGAGTACGCTTTTACTGAT	227		
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QY	288	GAAAGGGGGTTTAAATATCTACGGCTTATTTGTGAACGAATATTTATATGTGACAG	347		
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QY	348	ATTTGTTAAACAGCAATATATGTTTTTATTCGCTTTGCTGATTTTTCACATGTAACCT	407		
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QY	408	TCCAGTATCAACAGCGGTTACATTTGTCGTGTGACAGTAGCTATACACGTTACAGCGTGT	467		
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QY	468	TGCAGGATCATGTCGTATCGGGGATGACGATTAATTCGCATTTCGTTGACTTCTTATCT	527		
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QY	528	GGATTTAATGTCGATAGTGGAACTCTACTGACGCGAGCTGTGTGCAAGACGATGTTAG	587		
Db	19930	GGATTTAATGTCGATAGTGGAACTCTACTGACGCGAGCTGTGTGCAAGACGATGTTAG	19888		
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QY	708	ATTGAACCTGGGGAAGTTGATAGTACGCTCTGCTGATATCATGACGAAGACTCTGTTG	767		
Db	20010	ATTGAACCTGGGGAAGTTGATAGTACGCTCTGCTGATATCATGACGAAGACTCTGTTG	20066		
QY	768	TGTAGAGGAATTTCTTTTGGAGACTTAAATGCAATCTCGGAAAGCGGTGCATTAATCT	827		
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Oy		828	GAATTCGACATCAGCATCGGGAGTTGCCAAGAATGCATCGAGTTCCTTCAT	887
Db		20130	GAAATTGTCAATCAGCATCGGAATGCCAGATGGCATCTGATGATTCCTTCAT	20189
Oy		888	GTTCTCCGGCAGATGAGAAAGATCCGTGGGATTACGCACAATAAATATTTGGGATTCATC	947
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DB 2072 AACACTGATGATCTCAGTGGGCGTCTTATGATGATGCTGAGATGTTGATCTTAC 2131
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DB 2132 ATTGAACCTGGGGAAGTGTGAGTACGCTCTGCTGACTATCATGAGCAAGACTCTGTTG 2191
QY 768 TGTAGGAAGAAATTTCTTTTGGAGCAATTAATGCAATTTCTGGGAAGCGTGCATTAATCT 827
DB 2192 TGTAGGAAGAAATTTCTTTTGGAGCAATTAATGCAATTTCTGGGAAGCGTGCATTAATCT 2251
QY 828 GAATTTGATCATCATGATCATGCGAGTGGCCAGAAATGAGCATCTGATGATTTCTTCTAT 887
DB 2252 GAATTTGATCATCATGATCATGCGAGTGGCCAGAAATGAGCATCTGATGATTTCTTCTAT 2311
QY 888 GTGTCCGCGAGATGGAAGAGTCCGTGGGATTTACGCAATAAATATTTGGGATTCATC 947
DB 2312 GTGTCCGCGAGATGGAAGAGTCCGTGGGATTTACGCAATAAATATTTGGGATTCATC 2371
QY 948 CACTCTGGGGCAATTTCTGATGCGCAGCAACATTAATGACAGTGG 989
DB 2372 CACTCTGGGGCAATTTCTGATGCGCAGCAACATTAATGACAGTGG 2413
RESULT 10
AR099884 2127 bp DNA linear PAT 14-FEB-2001
LOCUS AR099884
DEFINITION Sequence 32 from patent US 6080400.
ACCESSION AR099884

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VERSION      AR099884.1  GI:12810332
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 2127)
AUTHORS      Williams, J.A. and Byrne, L.Marie.
TITLE        Compositions for the prevention and treatment of verotoxin-induced
              disease
JOURNAL      Patent: US 6080400-A 32 27-JUN-2000;
FEATURES     Location/Qualifiers
              1..2127
              source          /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      58.4%; Score 879.4; DB 2; Length 2127;
Best Local Similarity 99.3%; Pred. No. 8.5e-252;
Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 101 CAGATCTGAAGAAATTTACTTCTGCTGCTGCAAGAGAGCTATGATTCGCTGA 160
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DB 1238 CAGAAATTCAGGAATTTACTTCTGCTGCTGCAAGAGAGCTATGATTCGCTGA 1297

QY 161 ATGTCATTCGCTGCTGCAAGAGAGCTATTCATTAAGAGAGAGAGAGAGAGAG 220
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DB 1298 ATGTCATTCGCTGCTGCAAGAGAGCTATTCATTAAGAGAGAGAGAGAGAGAG 1357

QY 221 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 280
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DB 1358 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1417

QY 281 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 340
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DB 1418 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1477.

QY 341 TGACAGAGATTTGTTAAACAGAGCAAAATATGTTTTTATGCTTGGCTGATTTTTCATG 400
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DB 1478 TGACAGAGATTTGTTAAACAGAGCAAAATATGTTTTTATGCTTGGCTGATTTTTCATG 1537

QY 401 TTACCTTTCCAGGTACCAACAGCGGTTACATTTGCTGCTGCAAGTACTATACCACTTAC 460
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DB 1538 TTACCTTTCCAGGTACCAACAGCGGTTACATTTGCTGCTGCAAGTACTATACCACTTAC 1597

QY 461 AGGCTGTGAGAGGATAGTCGACAGCGGAGATGCAAGATAATTCGCTGCTGCACTACT 520
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DB 1598 AGGCTGTGAGAGGATAGTCGACAGCGGAGATGCAAGATAATTCGCTGCTGCACTACT 1657

QY 521 CTATCTGATTTAATGTCATAGTGAACCTTCACTGACGACAGTCTGTGGCAAGAGCGA 580
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DB 1658 CTATCTGATTTAATGTCATAGTGAACCTTCACTGACGACAGTCTGTGTGGCAAGAGCGA 1717

QY 581 TGTTCAGGTTTGTTCCTGTCACAGCTGAAGCTTTACGTTTTTGGCAATATCAAGAGGGAT 640
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DB 1718 TGTTCAGGTTTGTTCCTGTCACAGCTGAAGCTTTACGTTTTTGGCAATATCAAGAGGGAT 1777

QY 641 TTGCTAACAACTGAGATCTCAGTGGGGGCTTCTTATGTAATGACGCTGAAGATGTTG 700
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QY 701 ATCTTACATTGAACCTGGGGAAGGTTGAGTACGCTTCTGCTGACTATCATGACAAAGACT 760
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DB 1838 ATCTTACATTGAACCTGGGGAAGGTTGAGTACGCTTCTGCTGACTATCATGACAAAGACT 1897

QY 761 CTGTTCTGTGAGAAATTTCTTTTGAAGCATTTATGCAATTCCTGGGAAGGCTGGCAT 820
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DB 1898 CTGTTCTGTGAGAAATTTCTTTTGAAGCATTTATGCAATTCCTGGGAAGGCTGGCAT 1957

QY 821 TAAATACGAATGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 880
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DB 1958 TAAATACGAATGTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2017

QY 881 CTTCTATGTGTCCGGCAGATGAGAGAGTCCGTGGGATTAACGACAAATTAATTTGTGGG 940
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DB 2018 CTTCTATGTGTCCGGCAGATGAGAGAGTCCGTGGGATTAACGACAAATTAATTTGTGGG 2077
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QY 941 ATTCATTCACCTCTGGGGGCAATTCGATGCGCAGACACTATTAATGACGTGG 989
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DB 2078 ATTCATTCACCTCTGGGGGCAATTCGATGCGCAGACACTATTAATGACGTGG 2126
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RESULT 11
AR431418      2127 bp  DNA      linear  PAT 18-DEC-2003
LOCUS         Sequence 32 from patent US 6652857.
DEFINITION   AR431418
ACCESSION    AR431418
VERSION      AR431418.1  GI:40193454
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 2127)
AUTHORS      Williams, J.A., Byrne, L.M. and Pugh, C.S.G.
TITLE        Methods for producing avian verotoxin antitoxin
JOURNAL      Patent: US 6652857-A 32 25-NOV-2003;
              Promega Corporation; Madison, WI
FEATURES     Location/Qualifiers
              1..2127
              /organism="unknown"
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ORIGIN
Query Match      58.4%; Score 879.4; DB 2; Length 2127;
Best Local Similarity 99.3%; Pred. No. 8.5e-252;
Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 101 CAGATCTGAAGAAATTTACTTCTGCTGCTGCAAGAGAGCTATGATTCGCTGA 160
    |||
DB 1238 CAGAAATTCAGGAATTTACTTCTGCTGCTGCAAGAGAGCTATGATTCGCTGA 1297

QY 161 ATGTCATTCGCTGCTGCAAGAGAGCTATTCATTAAGAGAGAGAGAGAGAGAG 220
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DB 1298 ATGTCATTCGCTGCTGCAAGAGAGCTATTCATTAAGAGAGAGAGAGAGAGAG 1357

QY 221 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 280
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DB 1358 TACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1417

QY 281 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 340
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DB 1418 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1477

QY 341 TGACAGAGATTTGTTAAACAGAGCAAAATATGTTTTTATGCTTGGCTGATTTTTCATG 400
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DB 1478 TGACAGAGATTTGTTAAACAGAGCAAAATATGTTTTTATGCTTGGCTGATTTTTCATG 1537

QY 401 TTACCTTTCCAGGTACCAACAGCGGTTACATTTGCTGCTGCAAGTACTATACCACTTAC 460
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DB 1538 TTACCTTTCCAGGTACCAACAGCGGTTACATTTGCTGCTGCAAGTACTATACCACTTAC 1597

QY 461 AGGCTGTGAGAGGATAGTCGACAGCGGAGATGCAAGATAATTCGCTGCTGCACTACT 520
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DB 1598 AGGCTGTGAGAGGATAGTCGACAGCGGAGATGCAAGATAATTCGCTGCTGCACTACT 1657

QY 521 CTATCTGATTTAATGTCATAGTGAACCTTCACTGACGACAGTCTGTGGCAAGAGCGA 580
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DB 1658 CTATCTGATTTAATGTCATAGTGAACCTTCACTGACGACAGTCTGTGGCAAGAGCGA 1717

QY 581 TGTTCAGGTTTGTTCCTGTCACAGCTGAAGCTTTAGTTTTTGGCAATATCAAGAGGGAT 640
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DB 1718 TGTTCAGGTTTGTTCCTGTCACAGCTGAAGCTTTAGTTTTTGGCAATATCAAGAGGGAT 1777

QY 641 TTGCTAACAACTGAGATCTCAGTGGGGCTTCTTATGTAATGACGCTGAAGATGTTG 700
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DB 1778 TTGCTAACAACTGAGATCTCAGTGGGGCTTCTTATGTAATGACGCTGAAGATGTTG 1837
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QY	701	TTCTTAACTTGAACCTGGGAGAGCTTGACTGACCCCTCGCCGACATATCATGACAGACT	760
Db	1838	ATCTTACATTAACATCGGGAGAGGTGATGACCGTCTGCTGACATATCATGACAGACT	1897
QY	761	CTGTTCCGTGTGAGGAAGAAATTTCTTTTGGAGACATTTAATGCAATTCGTGGGAAGCGTGCGAT	820
Db	1898	CTGTTCCGTGTGAGGAAGAAATTTCTTTTGGAGACATTTAATGCAATTCGTGGGAAGCGTGCGAT	1957
QY	821	TAAATCTGAATTTGTCATATCATGATCGATCGGAGTTGCCAGATGGCATCTGATGAGTTTC	880
Db	1958	TAAATCTGAATTTGTCATATCATGATCGATCGGAGTTGCCAGATGGCATCTGATGAGTTTC	2017
QY	881	CTTCTATGTGTCGGCGACAGATGGAAGAGCCGTGGGAATTACGACACATPAAATATTTGGGG	940
Db	2018	CTTCTATGTGTCGGCGACAGATGGAAGAGCCGTGGGAATTACGACACATPAAATATTTGGGG	2077
QY	941	ATTCATTCACATCTCTGGGGGCGCAATTCCTGATCGCGACAACTATTAGCAGTGG	989
Db	2078	ATTCATTCACATCTCTGGGGGCGCAATTCCTGATCGCGACAACTATTAGCAGTGG	2126
RESULT 12			
LOCUS	AB030485	1238 bp	DNA linear BCT 06-JAN-2001
DEFINITION	Escherichia coli stx1 genes for Shiga-like toxin 1 A-subunit, Shiga-like toxin 1 B-subunit, complete cds.		
ACCESSION	AB030485	GI:12249025	
KEYWORDS	Shiga-like toxin 1 B-subunit; Shiga-like toxin 1 A-subunit.		
SOURCE	Escherichia coli		
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.		
REFERENCE	1 (bases 1 to 1238)		
AUTHORS	Sou-ichi,M.		
TITLE	Detection of Shiga-like Toxin Producing Escherichia coli from Seagulls		
JOURNAL	Published Only in Database (2001)		
REFERENCE	2 (bases 1 to 1238)		
AUTHORS	Sou-ichi,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-JUN-1999) Makino Sou-ichi, Obihiro University of Agriculture and Veterinary Medicine, Department of Veterinary Microbiology, Inada, Obihiro, Hokkaido 080-8535, Japan (E-mail:smakino@obihiro.ac.jp, URL:http://www.obihiro.ac.jp, Tel:81-155-49-5386, Fax:81-155-49-5402)		
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CDS			

ORIGIN	Query Match	58.3%	Score 879	DB 15	Length 1238
	Best Local Similarity	99.4%	Pred. No. 1.2e-251		
	Matches 882	Conservative 0	Mismatches 5	Indels 0	Gaps 0
QY	103 GATCTGAAGAAATTACTTCACTTCTGCAGCTGCAGCAAGCGTATGTAGATTCGCTGAT				162
DB	61 GTTCCGAAGAAATTACTTCACTTCTGCAGCTGCAGCAAGCGTATGTAGATTCGCTGAT				120
QY	163 GTCAATTCGCTCTGCATATAGGTACTCCATTAACAATAATTTATCAGAGGTACGCTTTTA				222
DB	121 GTCAATTCGCTCTGCATATAGGTACTCCATTAACAATAATTTATCAGAGGTACGCTTTTA				180
QY	223 CTGATGATTTGATATGTGCAACAGGGGAAATTTGTTTTCAGATGATATGTACAGAGGATATGAT				282
DB	181 CTGATGATTTGATATGTGCAACAGGGGAAATTTGTTTTCAGATGATATGTACAGAGGATATGAT				240
QY	283 CCAGAGGAAGGCGGTTTAATTAATCTACGCGCTTATTTGTGAAACGAAATTAATTTATATGTC				342
DB	241 CCAGAGGAAGGCGGTTTAATTAATCTACGCGCTTATTTGTGAAACGAAATTAATTTATATGTC				300
QY	343 ACAGAAATTTGTTAAACAGACAAATTAATGTTTTTATGCTTTGCTGATTTTTCACATGTT				402
DB	301 ACAGAAATTTGTTAAACAGACAAATTAATGTTTTTATGCTTTGCTGATTTTTCACATGTT				360
QY	403 ACCTTTCCAGGTAACAACAGGGGTTACATATGTCGTGTGACAGTACTATATACCACGTTACAG				462
DB	361 ACCTTTCCAGGTAACAACAGGGGTTACATATGTCGTGTGACAGTACTATATACCACGTTACAG				420
QY	463 CGTGTTCAGGGATCACTGTCGACGGGATGCGATTAATTCGCAATTCGCTTACTTACTTCT				522
DB	421 CGTGTTCAGGGATCACTGTCGACGGGATGCGATTAATTCGCAATTCGCTTACTTACTTCT				480
QY	523 TATCTGATTTAATGTGCGATATGTGGAACCTCACTGACGCGAGTCTGTGGAAGGCGATG				582
DB	481 TATCTGATTTAATGTGCGATATGTGGAACCTCACTGACGCGAGTCTGTGGAAGGCGATG				540
QY	583 TTACGGTTTGTACCTGTGACAGCTGAAAGCTTTACGTTTTCCGCAAAATACAGAGGGGATTT				642
DB	541 TTACGGTTTGTACCTGTGACAGCTGAAAGCTTTACGTTTTCCGCAAAATACAGAGGGGATTT				600
QY	643 CGTACACACTGTGATGATCTCAGTGGGGGTTCTTATGTAATGACCTGCTGGAAGATGTTGAT				702
DB	601 CGTACACACTGTGATGATCTCAGTGGGGGTTCTTATGTAATGACCTGCTGGAAGATGTTGAT				660
QY	703 CTTACATTTGAACGTGGGGAAGGTTGAGTACGCTCTGCTGACTATCATGACCAAGACTCT				762
DB	661 CTTACATTTGAACGTGGGGAAGGTTGAGTACGCTCTGCTGACTATCATGACCAAGACTCT				720
QY	763 GTTCGTGTAGGAAGAAATTTCTTTTGGANGACTTAATGCAATTTCTGGGAAGCGTGCATTA				822
DB	721 GTTCGTGTAGGAAGAAATTTCTTTTGGANGACTTAATGCAATTTCTGGGAAGCGTGCATTA				780
QY	823 ATATCGAATTTGTCATCATCATGATCGAGATGTGCGACAATGCGCTGATGAGTTTCT				882
DB	781 ATATCGAATTTGTCATCATCATGATCGAGATGTGCGACAATGCGCTGATGAGTTTCT				840
QY	883 TCTATGTCCTCGGAGATGGAAGAGTCCGTGGGATTTAGCGCACAATTAATATTTGGGAT				942
DB	841 TCTATGTCCTCGGAGATGGAAGAGTCCGTGGGATTTAGCGCACAATTAATATTTGGGAT				900
QY	943 TCATTCACCTCTGGGGGCAATTTCTGATGCGAGAACTTATAGCAGTTG 947				
DB	901 TCATTCACCTCTGGGGGCAATTTCTGATGCGAGAACTTATAGCAGTTG 947				

RESULT 13

SSO132761

LOCUS

DEFINITION

SSO132761

1362 bp

DNA

Shigella sonnei

linear

BCT 09-OCT-2000

stx and scx genes.

ACCESSION AJ132761
VERSION AJ132761.1 GI:4454334
KEYWORDS stx gene; stx protein; stx gene; stx protein.
SOURCE Shigella sonnei
ORGANISM Shigella sonnei
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
REFERENCE 1
AUTHORS Beutin, L., Struelens, E. and Fischer, I.
TITLE Isolation of Shigella sonnei lysozyme for a bacteriophage encoding gene for production of Shiga toxin
JOURNAL Lancet 353 (9163), 1498 (1999)
PUBMED 10232325
REFERENCE 2 (bases 1 to 1362)
AUTHORS Beutin, L.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1999) Beutin L., Emerging Bacterial Pathogens, Robert Koch Institut, Nordufer 20, D-13353 Berlin, GERMANY
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ORIGIN
Query Match 58.3%; Score 879; DB 15; Length 1362;
Best Local Similarity 99.4%; Pred. No. 1.2e-251;
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 103 GATCTGAAGAAATTACCTTAGACTTCTGACGCAAGACGATGATGATGCTGGAAT 162
DB 154 GTTCCGAGGAATTTACTTACCTTCTGACGCAAGACGATGATGATGCTGGAAT 213
QY 163 GATCTGCTCTGCAATAGTACCTTACCTTACGATGATGATGATGATGATGATGAT 222
DB 214 GTATTCGCTCTGCAATAGTACCTTACCTTACGATGATGATGATGATGATGATGAT 273
QY 223 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
DB 274 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 333

QY 283 CCAGAGGAGGCGGCTTTAATATCTACGCTTATTTGTTGAACGAATATTTATATG 342
DB 334 CCAGAGGAGGCGGCTTTAATATCTACGCTTATTTGTTGAACGAATATTTATATG 393
QY 343 ACAGATTTGTTAACAAGCAATATATGTTTATTCCTTTCGTTGATTTTCAATGTT 402
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QY 403 ACCCTTCCAGGTACCAACAGCGGTTACCTTTCGTTGATGATGATGATGATGATGAT 462
DB 454 ACCCTTCCAGGTACCAACAGCGGTTACCTTTCGTTGATGATGATGATGATGATGAT 513
QY 463 CGTGTGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 522
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QY 523 TATCTGATTTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 582
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QY 943 TCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
DB 994 TCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040
RESULT 14
SHEPST 1500 bp DNA linear BCT 21-APR-1996
LOCUS S.dysenteriae type 1 Shiga toxin alpha and beta subunit (stx) and
DEFINITION stx genes, complete cds.
ACCESSION M19437.1 GI:152784
VERSION M19437.1
KEYWORDS Shiga toxin.
SOURCE Shigella dysenteriae
ORGANISM Shigella dysenteriae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
REFERENCE 1 (bases 1 to 1500)
AUTHORS Strookbine, N.A., Jackson, M.P., Sung, L.M., Holmes, R.K. and O'Brien, A.D.
TITLE Cloning and sequencing of the genes for Shiga toxin from Shigella
JOURNAL J. Bacteriol. 170 (3), 1116-1122 (1988)
PUBMED 2830229
COMMENT Original source text: Shigella dysenteriae (clone: pNBS13.) DNA.
Draft entry and computer-readable sequence for (1) kindly provided
by M.Jackson, 02-JUN-1988.
FEATURES
Location/Qualifiers

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	YLDLMSHSGTSLTQSVARAMLRFVTVAEALRFQIQKGFETLIDLSGRSVYVTAED	
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ORIGIN	726 bp upstream of HindIII site.	
Query Match	58.3%; Score 879; DB 15; Length 1500;	
Best Local Similarity	99.4%; Pred. No. 1.1e-251;	
Matches	882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	103 GATCTGAAGAAATTTACCTTAGACTCTTCGACTCGCAAGACGTATGTAGATTCCGCTGAAT	162
DB	111	
DB	221 GTTGGGAAGAAATTTACCTTAGACTCTTCGACTCGCAAGACGTATGTAGATTCCGCTGAAT	280
QY	163 GTCATTGCTCTGCATATAGTACTCCATTCATTAAGACTATTTTCATCGAAGATACGCTCTT	222
DB	281 GTCATTGCTCTGCATATAGTACTCCATTCATTAAGACTATTTTCATCGAAGATACGCTCTT	340
QY	223 CTGATGATTGATAGTGGACAGAGGGATTAATTTGTTGCAAGTTGATGTCAAGAGATTAAT	282
DB	341 CTGATGATTGATAGTGGACAGAGGGATTAATTTGTTGCAAGTTGATGTCAAGAGATTAAT	400
QY	283 CCAGAGGAAGCGGCTTTAATATATACGGCTATTTGTTGAACGAATTAATTAATATG	342
DB	401 CCAGAGGAAGCGGCTTTAATATATACGGCTATTTGTTGAACGAATTAATTAATATG	460
QY	343 ACAGAGATTGTTAAACAGCAAAATATGTTTTTATCGCTTGCATATTTTTCACATGTT	402
DB	461 ACAGAGATTGTTAAACAGCAAAATATGTTTTTATCGCTTGCATATTTTTCACATGTT	520
QY	403 ACCTTTCCAGGTACAAACAGCGGTACATTTGTCGTGACAGTACGATTAACACGTTACAG	462
DB	521 ACCTTTCCAGGTACAAACAGCGGTACATTTGTCGTGACAGTACGATTAACACGTTACAG	580

OY		463	CGGTTCCAGGGAACTCATTCGAACGGGGATGCAGATAAATGCCATTGCTTGACTCACTTCT	522
Db		581	CGTGTTCAGAGGATCAGTCGTAACGGGATGCAGATAAATGCCATTGCTTGACTCACTTCT	640
OY		523	TATCTGGATTAAATGTGCGATAGTGAACCTCACTGACGCAAGTCTGTGGCAAGGCATG	582
Db		641	TATCTGGATTAAATGTGCGATAGTGAACCTCACTGACGCAAGTCTGTGGCAAGGCATG	700
OY		583	TTAACGTTTTGTACTGTGACACGCTGAACCTTACGTTTGGGCAATAACAGAGGGATTT	642
Db		701	TTAGCGTTTTGTACTGTGACACGCTGAACCTTACGTTTGGGCAATAACAGAGGGATTT	760
OY		643	CGTACAACACCTGAGTAGATCTCAGTGGGCGTCTTATGTAAATGACTGTGAGAATGTTGAT	702
Db		761	CGTACAACACCTGAGTAGATCTCAGTGGGCGTCTTATGTAAATGACTGTGAGAATGTTGAT	820
OY		703	CTTACATTGAACCTGGGGAAGGTGATGAGCGTCTGCTGACTATCATGACAAAGACTCT	762
Db		821	CTTACATTGAACCTGGGGAAGGTGATGAGCGTCTGCTGACTATCATGACAAAGACTCT	880
OY		763	GTTGCGTAGGAAGAAATTTCTTTTGAAGACTTATATGCAATTTCTGGGAAGCGTGGCATTA	822
Db		881	GTTGCGTAGGAAGAAATTTCTTTTGAAGACTTATATGCAATTTCTGGGAAGCGTGGCATTA	940
OY		823	ATACTGAATGTCTCATCATCATGATCATCGGAGTTGCCAGATGSCATCTGATGATTTCT	882
Db		941	ATACTGAATGTCTCATCATCATGATCATCGGAGTTGCCAGATGSCATCTGATGATTTCT	1000
OY		883	TCTATGTGTCGGGAGATGAAAGATCCGTGGGATTTACGCAATPAATAATTTGTGGGAT	942
Db		1001	TCTATGTGTCGGGAGATGAAAGATCCGTGGGATTTACGCAATPAATAATTTGTGGGAT	1060
OY		943	TCATCCACTCTGGGGGCAATTCGTATGTCGCAAGACTATTACAGTGG	989
Db		1061	TCATCCACTCTGGGGGCAATTCGTATGTCGCAAGACTATTACAGTGG	1107
RESULT 15				
AF461172				
LOCUS				
DEFINITION			1956 bp DNA linear BCT 01-JUL-2002	
			Escherichia coli PDJ30 Shiga toxin 1A subunit (stx1A) and Shiga	
			toxin 1B subunit (stxB) genes, complete cds.	
ACCESSION			AF461172	
VERSION			AF461172.1	
KEYWORDS			GI:21636532	
SOURCE				
ORGANISM			Escherichia coli	
			Escherichia coli	
			Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
			Enterobacteriaceae; Escherichia.	
REFERENCE			1 (bases 1 to 1956)	
AUTHORS			Yu,J.Y., Jeon,H.G., Kang,Y.H., Kim,E.C., Sohn,C.K. and Lee,B.K.	
TITLE			Characterization of Shiga toxin genes in Shiga toxin-producing	
JOURNAL			Escherichia coli isolated in Korea	
FEATURES			Unpublished	
source			2 (bases 1 to 1956)	
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			/serotype="O26:H4"	
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			/transl_table=11	
gene				
CDS				

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/product="Shiga toxin 1A subunit"
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YLDLMHSGSTLSQSVARAMLREVTVAALRFRJOROFRITLDDLSGRSVYMAED
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/translation="MKITILIASLSPFSALATPDVTKVEYTKYNDDETIVKV
GDKELFTNRMNIQSLILSAQITGMVTITIKINACHNGGSEVIFR"

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ORIGIN

Query Match 58.3%; Score 879; DB 15; Length 1956;

Best Local Similarity 99.4%; Pred. No. 1,1e-251;

Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 103 GATCTGAAGAATTACTTACTAGACTCTGCTGCAAGCAAGAGATGATGATGCTGAAT 162
DB 748 GTTGCGAAGAAATTACTTACTAGACTCTGCTGCAAGCAAGAGATGATGATGCTGAAT 807
QY 163 GTCATTGCTCTGCAATAGGTAATCTCAATTAACAATATTTTCATCAGAGGTAAGTCTTTA 222
DB 808 GTCAATGCTCTGCAATAGGTAATCTCAATTAACAATATTTTCATCAGAGGTAAGTCTTTA 867
QY 223 CTGATGATTAATAGTGCAACAGGGGAATATTTGTTGCACTGATGATGCAAGGATAGAT 282
DB 868 CTGATGATTAATAGTGCAACAGGGGAATATTTGTTGCACTGATGATGCAAGGATAGAT 927
QY 283 CCAGAGAGAGGGCGTTAATTAATCTACGGCTTAATTTGTAACAAATAATTTATATG 342
DB 928 CCAGAGAGAGGGCGTTAATTAATCTACGGCTTAATTTGTAACAAATAATTTATATG 987
QY 343 ACAGGATTTGTTAACAAGCAATATGTTTTTATGCTTGTGATTTTTCATATG 402
DB 988 ACAGGATTTGTTAACAAGCAATATGTTTTTATGCTTGTGATTTTTCATATG 1047
QY 403 ACCTTTCAGGTACAACAGGGTTACATGCTGCTGAGACAGTACGCTATACAGTTACAG 462
DB 1048 ACCTTTCAGGTACAACAGGGTTACATGCTGCTGAGACAGTACGCTATACAGTTACAG 1107
QY 463 CGTGTTCAGGATCAGTCTGACGGGATGCAATTAATCGCAATTCGTTGACTACTTCT 522
DB 1108 CGTGTTCAGGATCAGTCTGACGGGATGCAATTAATCGCAATTCGTTGACTACTTCT 1167
QY 523 TATCTGATTTAATGTCATAGTGAACCTCACTGACGAGTCTGTCGAAGGCGATG 582
DB 1168 TATCTGATTTAATGTCATAGTGAACCTCACTGACGAGTCTGTCGAAGGCGATG 1227
QY 583 TTACGTTTGTACGACAGCTGAAGCTTTACGTTTTCGGCAATAATACAGAGGGGATTT 642
DB 1228 TTACGTTTGTACGACAGCTGAAGCTTTACGTTTTCGGCAATAATACAGAGGGGATTT 1287
QY 643 CGTACAACACTGATGATCTCAGTGGGCGTTCTTATGTAATGACTGCTGAAGATGTTGAT 702
DB 1288 CGTACAACACTGATGATCTCAGTGGGCGTTCTTATGTAATGACTGCTGAAGATGTTGAT 1347
QY 703 CTTACATTGAACCTGGGAAGGTTGATGAGCTCTGCTGATCACTATGACAAAGACTCT 762
DB 1348 CTTACATTGAACCTGGGAAGGTTGATGAGCTCTGCTGATCACTATGACAAAGACTCT 1407
QY 763 GTTCGTGAGAGAAATTTCTTTTGAAGCAATTAATGCAATTCGGAAGCGTGGCATTA 822
DB 1408 GTTCGTGAGAGAAATTTCTTTTGAAGCAATTAATGCAATTCGGAAGCGTGGCATTA 1467

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QY 823 ATACTGAATTCATCATCATGATCGGAGTTGCCAAGATGCGATGATGATTTTCT 882
DB 1468 ATACTGAATTCATCATCATGATCGGAGTTGCCAAGATGCGATGATGATGATTTTCT 1527
QY 883 TCTATGTTCCGGCAGATGGAAGCTCCGTGGGATTTACCGCAATTAATAATTTGGGAT 942
DB 1528 TCTATGTTCCGGCAGATGGAAGCTCCGTGGGATTTACCGCAATTAATAATTTGGGAT 1587
QY 943 TCATCCACTCTGGGGCAATTCGTATGCGCAGAACTATTAACAGTGG 989
DB 1588 TCATCCACTCTGGGGCAATTCGTATGCGCAGAACTATTAACAGTGG 1634

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Search completed: January 23, 2007, 04:04:22
Job time : 8801 secs

PT Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial infections
PT comprises expression vector encoding bacterial toxin.

CC verotoxins are useful as immunogens for the production of vaccines,
 CC including multivalent vaccines and antitoxins, which can be administered
 CC to a subject at risk of diarrhoeal disease or at risk of developing extra
 CC -intestinal complications of E. coli infections, e.g. haemolytic uremic
 CC syndrome, thrombotic thrombocytopenic purpura. The present sequence
 CC represents the cDNA encoding the MBPvtx1-A protein #2 of the invention.
 CC This fusion protein was created to facilitate purification of the
 CC recombinant proteins of the invention
 CC
 XX

Sequence 2073 BP, 578 A, 448 C, 535 G, 512 T, 0 U, 0 Other;

Query Match 58.5%; Score 881.4; DB 6; Length 2073;

Best Local Similarity 99.3%; Pred. No. 1.2e-253;

Matches 885; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 99 CCCAGATCTGAAGAAATTACCTTAGACTTCTGCAGCTGCAAGACGATGATGATGGCT 158
DB 1182 CCGGGAATTCAAGAAATTACCTTAGACTTCTGCAGCTGCAAGACGATGATGATGGCT 1241
QY 159 GAATGTCATTCGCTCTGCAATAGGACTCCATTCAGACTATTCATCAGAGGATGCTC 218
DB 1242 GAATGTCATTCGCTCTGCAATAGGACTCCATTCAGACTATTCATCAGAGGATGCTC 1301
QY 219 TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
DB 1302 TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1361
QY 279 AGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 338
DB 1362 AGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1421
QY 339 TGTGACAGGATTTGTTAAGACAGACAAATATGTTTATGCTGCTGCTGCTGCTGCT 398
DB 1422 TGTGACAGGATTTGTTAAGACAGACAAATATGTTTATGCTGCTGCTGCTGCTGCT 1481
QY 399 TGTTCACCTTTCAGGTACACAGCGGTTACATTTGCTGCTGCTGCTGCTGCTGCT 458
DB 1482 TGTTCACCTTTCAGGTACACAGCGGTTACATTTGCTGCTGCTGCTGCTGCTGCT 1541
QY 459 ACAGGCTGTTGAGGAGGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 518
DB 1542 ACAGGCTGTTGAGGAGGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1601
QY 519 TTTCTATCTGATTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
DB 1602 TTTCTATCTGATTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1661
QY 579 GATGTTACGGTTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 638
DB 1662 GATGTTACGGTTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1721
QY 639 ATTGCTGACACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 698
DB 1722 ATTGCTGACACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1781
QY 699 TGATCTTACATTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 758
DB 1782 TGATCTTACATTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1841
QY 759 CTCTGTTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 818
DB 1842 CTCTGTTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1901
QY 819 ATTAATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
DB 1902 ATTAATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1961
QY 879 TCTCTTATGATGCTCGGAGATGAGAGATCGGTGGGATTTACGCAATTAATATGTTG 938
DB 1962 TCTCTTATGATGCTCGGAGATGAGAGATCGGTGGGATTTACGCAATTAATATGTTG 2021
QY 939 GGATTCATCACTCTGGGGGCAATTGTGATGGCGAGAACTTATAGCAGTGG 989
  
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DB 2022 GGATTCATCACTCTGGGGGCAATTGTGATGGCGAGAACTTATAGCAGTGG 2072

RESULT 3

AA227687
 AA227687 standard; DNA; 1369 BP.

AA227687;

22-DEC-1999 (first entry)

Verotoxin 1 gene.

Verotoxin; VT1; VT2; detection; PCR primer; ss.

Escherichia coli.

JP11243996-A.

14-SEP-1999.

27-FEB-1998; 98UP-00047677.

27-FEB-1998; 98UP-00047677.

(TOYM) TOYOBO KK.

WP1; 1999-603716/52.

An oligonucleotide for amplification of verotoxin - useful in the detection of inactivated verotoxin gene by transfer of a foreign DNA fragment.

Claim 1; Page 8; 10pp; Japanese.

This sequence represents the Escherichia coli verotoxin1 (VT1) gene. The invention relates to an oligonucleotide for amplification of VT. The oligonucleotide is useful for detection of inactivated VT gene by transfer of a foreign DNA fragment. Simple, rapid and specific amplification of VT gene from environmental factors is achieved using the oligonucleotide of the invention

Sequence 1369 BP, 379 A, 225 C, 330 G, 435 T, 0 U, 0 Other;

Query Match 58.4%; Score 880.4; DB 2; Length 1369;

Best Local Similarity 99.9%; Pred. No. 1.8e-253;

Matches 881; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 108 GAAGGAATTTACCTTAACTTCTGACTGCAAGACGATGATGATGATGATGATGAT 167
DB 98 GAAGGAATTTACCTTAACTTCTGACTGCAAGACGATGATGATGATGATGATGAT 157
QY 168 TCGCTGCAATAGGATCTCCATTCAGACTATTTCAATCAGAGGATGATGATGAT 227
DB 158 TCGCTGCAATAGGATCTCCATTCAGACTATTTCAATCAGAGGATGATGATGAT 217
QY 228 GATTGATAGTGCACAGGAGGATTAATTTGTCAGTTGATGTCAGAGGATGATGAT 287
DB 218 GATTGATAGTGCACAGGAGGATTAATTTGTCAGTTGATGTCAGAGGATGATGAT 277
QY 288 GGAAGGGGGGTTTAAATATCTACAGGCTTATGTTGAAGCAATTAATTAATGAGCAG 347
DB 278 GGAAGGGGGGTTTAAATATCTACAGGCTTATGTTGAAGCAATTAATTAATGAGCAG 337
QY 348 ATTGTTACAGAGCAATTAATGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 407
DB 338 ATTGTTACAGAGCAATTAATGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397
QY 408 TCCAGGTACCAACAGGGTTACATTTGCTGAGACATGCTATACAGGATTAACAGGCTGT 467
DB 398 TCCAGGTACCAACAGGGTTACATTTGCTGAGACATGCTATACAGGATTAACAGGCTGT 457
QY 468 TCCAGGTACATGCTATACGGGGATGACAGATTAATGATGATGATGATGATGATGAT 527
  
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Db 458 TCGAGGATCATGTCGAGGGGATGCGAATAATCCGATTCCTGATCTATATCT 517
Qy 528 GATTTAAATGTCGATAGTGAACCTCAGACGAGCGTCGTGGCAAGCCGATGTAG 587
Db 518 GGAATTTAAATGTCGATAGTGAACCTCAGACGAGCGTCGTGGCAAGCCGATGTAG 577
Qy 588 GTTGTACTGTGACAGCTGAAGCTTTCCTTTTCGCAAAATACAGAGGGGATTTGTCAC 647
Db 578 GTTGTACTGTGACAGCTGAAGCTTTCCTTTTCGCAAAATACAGAGGGGATTTGTCAC 637
Qy 648 AACACTGATGATCTCAGTGGGCGTCTTATGTAAAGCTGCTGAAGATTTGATCTTAC 707
Db 638 AACACTGATGATCTCAGTGGGCGTCTTATGTAAAGCTGCTGAAGATTTGATCTTAC 697
Qy 708 ATTGAAGTGGGGAAGGTGAGTAGCGCTGCTGATATCATGACCAAGACTCTGTG 767
Db 698 ATTGAAGTGGGGAAGGTGAGTAGCGCTGCTGATATCATGACCAAGACTCTGTG 757
Qy 768 TGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAAAGCGTGGCATTAATCT 827
Db 758 TGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAAAGCGTGGCATTAATCT 817
Qy 828 GAATTTGTCATCATGATGATCGGAGATTTGCCAAGATGGCATCTGATGATTTCTTCTAT 887
Db 818 GAATTTGTCATCATGATGATCGGAGATTTGCCAAGATGGCATCTGATGATTTCTTCTAT 877
Qy 888 GTGTCCGGGAGATGGAAGAGTCCGTGGGATTAAGCAAAATTAATTTGGGATTCATC 947
Db 878 GTGTCCGGGAGATGGAAGAGTCCGTGGGATTAAGCAAAATTAATTTGGGATTCATC 937
Qy 948 CACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 989
Db 938 CACTCTGGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 979

RESULT 4
ID ADL25576 standard; DNA; 1227 BP.
XX AC ADL25576;
XX DT 20-MAY-2004 (first entry)
XX DE S. dysenteriae shiga toxin gene stx-dysenteriae.
XX KM Shiga toxin; ds; gene; fluorescence resonance energy transfer; FRET;
XX KM gastrointestinal disease; dysentery.
XX OS Shigella dysenteriae.
XX PN US2003215814-A1.
XX PD 20-NOV-2003.
XX PF 17-MAY-2002; 2002US-00150792.
XX PR 17-MAY-2002; 2002US-00150792.
XX PA (COCK/) COCKERILL F R.
XX PA (ROSE/) ROSENBLATT J E.
XX PA (SLOAN/) SLOAN L.
XX PA (UHLJ/) UHL J R.
XX PI Cockerill FR, Rosenblatt JE, Sloan L, Uhl JR;
XX DR WPI; 2003-902026/82.
XX PT Detecting presence or absence of Shiga toxin producing organisms in
XX PT biological sample, by amplifying nucleic acid encoding Shiga toxin with
XX PT pair of stx1 primers and detecting fluorescence resonance energy
XX PT transfer.
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PS Example 2; Fig 1; 24pp; English.
XX The invention relates to detecting the presence or absence of Shiga toxin
CC or Shiga-like toxin producing organisms in a biological sample involving
CC amplifying nucleic acid encoding Shiga toxin with a pair of stx1 primers,
CC detecting the amplified product with labelled stx1 probes, and detecting
CC the presence or absence of fluorescence resonance energy transfer (FRET).
CC Also included is an article of manufacture comprising the stx1 primers
CC and probes and a donor fluorescent moiety and corresponding fluorescent
CC moiety or a pair of stx2 primers, a pair of stx2 probes and a donor
CC fluorescent moiety and corresponding fluorescent moiety. The method is
CC useful for detecting the presence or absence of one or more Shiga toxin
CC or Shiga-like toxin producing organism e.g. Escherichia coli (especially
CC gastrointestinal disease causing strains) and Shigella (causative agent
CC of dysentery) in a biological sample which is a stool sample or body
CC fluids from an individual. The method is rapid and specific in detecting
CC the Shiga toxin from biological samples. The present sequence is a
CC bacterial shiga toxin or shiga-like toxin gene used to design the primers
CC and probes of the invention.
XX SQ Sequence 1227 BP; 334 A; 204 C; 298 G; 389 T; 0 U; 2 Other;

Query Match 58.4%; Score 879.6; DB 11; Length 1227;
Best Local Similarity 99.7%; Pred. No. 36-253; Indels 0; Gaps 0;
Matches 879; Conservative 2; Mismatches 1;

Qy 108 GAAGAAATTTACCTTAGACTTCTGACGTCGAAGAAGCTATGATGCTGAATGCTAT 167
Db 66 GAAGAAATTTACCTTAGACTTCTGACGTCGAAGAAGCTATGATGCTGAATGCTAT 125
Qy 168 TGCTCTGCAATAGGATCTCCATTTACAGCTATTTTCATAGAGAGATGCTTTACTGAT 227
Db 126 TGCTCTGCAATAGGATCTCCATTTACAGCTATTTTCATAGAGAGATGCTTTACTGAT 185
Qy 228 GATTGATAGTGGACAGCGGATTAATTTGTTGCAAGTATGTCAGAGGATAGATCCAGA 287
Db 186 GATTGATAGTGGACAGCGGATTAATTTGTTGCAAGTATGTCAGAGGATAGATCCAGA 245
Qy 288 GGAAGGGCGTTTAAATATCTACGCGTTATGTTGTAAGCAAAATTAATTAATGTCAGG 347
Db 246 GGAAGGGCGTTTAAATATCTACGCGTTATGTTGTAAGCAAAATTAATTAATGTCAGG 305
Qy 348 ATTGTTAACAGAGCAAAATTAATGTTTATGCTTGCTGATTTTTCATAGTTACCTT 407
Db 306 ATTGTTAACAGAGCAAAATTAATGTTTATGCTTGCTGATTTTTCATAGTTACCTT 365
Qy 408 TCCAGGTACAGACAGCGTTACATTTGTCGTGATGACAGTATACCTTACAGCGTGT 467
Db 366 TCCAGGTACAGACAGCGTTACATTTGTCGTGATGACAGTATACCTTACAGCGTGT 425
Qy 468 TCGAGGATCAAGTCTGATCGGGGATGCGAATAATGCGCATTTGTTGACTACTTCTTATCT 527
Db 426 TCGAGGATCAAGTCTGATCGGGGATGCGAATAATGCGCATTTGTTGACTACTTCTTATCT 485
Qy 528 GATTTAAATGTCGATAGTGAACCTCAGACGAGCGTCGTGGCAAGCCGATGTAG 587
Db 486 GATTTAAATGTCGATAGTGAACCTCAGACGAGCGTCGTGGCAAGCCGATGTAG 545
Qy 588 GTTGTACTGTGACAGCTGAAGCTTTCCTTTTCGCAAAATACAGAGGGGATTTGTCAC 647
Db 546 GTTGTACTGTGACAGCTGAAGCTTTCCTTTTCGCAAAATACAGAGGGGATTTGTCAC 605
Qy 648 AACACTGATGATCTCAGTGGGCGTCTTATGTAAAGCTGCTGAAGATTTGATCTTAC 707
Db 606 AACACTGATGATCTCAGTGGGCGTCTTATGTAAAGCTGCTGAAGATTTGATCTTAC 665
Qy 708 ATTGAAGTGGGGAAGGTGAGTAGCGCTGCTGATATCATGACCAAGACTCTGTG 767
Db 666 ATTGAAGTGGGGAAGGTGAGTAGCGCTGCTGATATCATGACCAAGACTCTGTG 725
Qy 768 TGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAAAGCGTGGCATTAATCT 827
Db 726 TGTAGAGAAATTTCTTTTGAAGCATTAATGCAATTTCTGGAAAGCGTGGCATTAATCT 785
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QY 828 GAATGTCATCATCATGATCGGAGTTCGACGAATGGCATCTGATGAGTTTCCCTCAT 887
 DB 786 GAATGTCATCATCATGATCGGAGTTCGACGAATGGCATCTGATGAGTTTCCCTCAT 845
 QY 888 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACAAATTAATATGTTGGGATTTCATC 947
 DB 846 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACAAATTAATATGTTGGGATTTCATC 905
 QY 948 CACTCTGGGGGCAATTTCTGATGCGGACGAATCTATTGCGAGTGG 989
 DB 906 CACTCTGGGGGCAATTTCTGATGCGGACGAATCTATTGCGAGTGG 947

RESULT 5

AEE48612

ID AEE48612 standard; DNA; 1227 BP.

AC AEE48612;

DT 23-FEB-2006 (first entry)

DE Shigella dysenteriae shiga-like toxin gene stx-dysenteriae.

XX Microorganism detection; Shiga-like toxin; gene; ds.

OS Shigella dysenteriae.

PN US2005282194-A1.

XX 22-DEC-2005.

PF 29-APR-2005; 2005US-00117858.

PR 17-MAY-2002; 2002US-00150792.

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

PI Cockerill FR, Rosenblatt JE, Sloan LM, Uhl JR;

DR WPI; 2006-046433/05.

PT Detecting Shiga-like toxin-producing organisms in sample, by detecting
 fluorescence resonance energy transfer between probes after amplifying
 PT and hybridizing toxin nucleic acid in sample with toxin specific primers
 PT and labeled probes.

PS Example 2; Fig 1; 25pp; English.

XX The present invention relates to a method (M1) for detecting the presence
 CC or absence of Shiga toxin (stx)- or Shiga-like toxin (stxl/stx2)-
 CC producing organisms in sample. The method comprises performing cycling
 CC step comprising amplifying and hybridizing steps, using sample, primers
 CC and labeled probes for nucleic acid molecule encoding the toxin, and
 CC detecting presence of fluorescence resonance energy transfer (FRET)
 CC between donor fluorescent moiety of first probe and acceptor fluorescent
 CC moiety of second probe. The present sequence is a Shiga-like toxin which
 CC was used in a sequence homology alignment to illustrate the invention.

SQ Sequence 1227 BP; 334 A; 204 C; 298 G; 389 T; 0 U; 2 Other;

Query Match 58.4%; Score 879.6; DB 15; Length 1227;

Best Local Similarity 99.7%; Pred. No. 36-253;

Matches 879; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACTAGACTTCTCGACTGCAAGACGATGATGATGCGTGAATGATCAT 167
 DB 66 GAAGGAATTTACTAGACTTCTCGACTGCAAGACGATGATGATGCGTGAATGATCAT 125
 QY 168 TCGCTCTGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 227
 DB 126 TCGCTCTGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 185

QY 228 GATTGATAGTGGCAGACAGGGGATTAATTTGTTGACGTTGATGTCAGAGGGATGATCCAGA 287
 DB 186 GATTGATAGTGGCAGACAGGGGATTAATTTGTTGACGTTGATGTCAGAGGGATGATCCAGA 245
 QY 288 GGAAGGCGGTTTAAATATCTACGCGCTTATTTGTAAGCAATTAATTAATGATGACAGG 347
 DB 246 GGAAGGCGGTTTAAATATCTACGCGCTTATTTGTAAGCAATTAATTAATGATGACAGG 305
 QY 348 ATTGTTAAGCAGCAATTAATGTTTAAATGCTTTGATGCTGATTTTCAATGTTACTCT 407
 DB 306 ATTGTTAAGCAGCAATTAATGTTTAAATGCTTTGATGCTGATTTTCAATGTTACTCT 365
 QY 408 TCCAGTACAAACAGCGGTTACATTTGCTGTGACAGTATTAACACGTTACAGCGTGT 467
 DB 366 TCCAGTACAAACAGCGGTTACATTTGCTGTGACAGTATTAACACGTTACAGCGTGT 425
 QY 468 TGCAGGATCAGTGTGTCGGGAGATGACAGTAAATCCGATTCGTTGACTACTCTTATCT 527
 DB 426 TGCAGGATCAGTGTGTCGGGAGATGACAGTAAATCCGATTCGTTGACTACTCTTATCT 485
 QY 528 GGATTTAATGTCGATATGAGGAACTCTCACTGACGCGAGTGTGCAAGAGCGATGTTACG 587
 DB 486 GGATTTAATGTCGATATGAGGAACTCTCACTGACGCGAGTGTGCAAGAGCGATGTTACG 545
 QY 588 GTTGTACTGTGACAGCTGAAAGCTTTACGTTTTCGGCAATACAGAGGGGATTTCTTAC 647
 DB 546 GTTGTACTGTGACAGCTGAAAGCTTTACGTTTTCGGCAATACAGAGGGGATTTCTTAC 605
 QY 648 AACACTGATGATGTCAGTGGGCGTTCTTAAATGATGACGCTGAAAGTGTGATCTTAC 707
 DB 606 AACACTGATGATGTCAGTGGGCGTTCTTAAATGATGACGCTGAAAGTGTGATCTTAC 665
 QY 708 ATTGAACGCGGGAAGTTGATGAGCTGCTGCTGCTGATCATGATGACAAAGACTGTTG 767
 DB 666 ATTGAACGCGGGAAGTTGATGAGCTGCTGCTGCTGATCATGATGACAAAGACTGTTG 725
 QY 768 TGTAGGAAGAAATTTCTTTGGAAGCATTAATGCAATTTCTGGAAAGCGTGGCATTAATCT 827
 DB 726 TGTAGGAAGAAATTTCTTTGGAAGCATTAATGCAATTTCTGGAAAGCGTGGCATTAATCT 785
 QY 828 GAATGTCATCATCATGATCGGAGTTCGACGAATGGCATCTGATGAGTTTCCCTCAT 887
 DB 786 GAATGTCATCATCATGATCGGAGTTCGACGAATGGCATCTGATGAGTTTCCCTCAT 845
 QY 888 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACAAATTAATATGTTGGGATTTCATC 947
 DB 846 GTGTCGGGAGATGAGAGAGTCCGTGGGATTACGACAAATTAATATGTTGGGATTTCATC 905
 QY 948 CACTCTGGGGGCAATTTCTGATGCGGACGAATCTATTGCGAGTGG 989
 DB 906 CACTCTGGGGGCAATTTCTGATGCGGACGAATCTATTGCGAGTGG 947

RESULT 6

ID AAV11404 standard; DNA; 1235 BP.

AC AAV11404;

DT 18-AUG-1998 (first entry)

DE Shiga toxin type 1 PCR fragment p7H1.

KW Histone-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;

KM haemorrhagic colitis; haemolytic uremic syndrome; ss.

OS Shigella dysenteriae.

PN W09811229-A2.

PD 19-MAR-1998.

PF 09-SEP-1997; 97WO-US015836.

	Best Local Similarity 99.3%; Pred. No. 4.7e-253; Matches 883; Conservative 0; Mismatches 6; Indels 0; Gaps 0.	
OY	101 CAGATCTGAAGGAATTACCTTTAGACTCTTCGACTGCAGAAAGCGTATGTAGATTGCTGA	160
Db	1238 CAGAAATTCAGAGGAATTTACCTTTAGACTCTTCGACTGCAGAAAGCGTATGTAGATTGCTGA	1297
OY	161 ATGTCAATTCGGCTCTGCAATAGGACTTCGATTACAGACATATTTCACAGAGGTAAGCTTT	220
Db	1238 ATGTCAATTCGGCTCTGCAATAGGACTTCGATTACAGACATATTTCACAGAGGTAAGCTTT	1357
OY	221 TACTGATGATTGATAGTAGGCAACAGGGGATAATTTGTTTGCAGTTGATGTCAAGAGATAG	280
Db	1358 TACTGATGATTGATAGTAGGCTCAGGGGATAATTTGTTTGCAGTTGATGTCAAGAGATAG	1417
OY	281 ATCCAGAGGAAGGGCGGTTTTTAATATCTACGGCTTATTTGTAACGAATAATTATATAG	340
Db	1418 ATGCAGAGGAAGGGCGGTTTTTAATATCTACGGCTTATTTGTAAGGAATAATTAATATAG	1477
OY	341 TGACAGAGATTTGTTTAAACAGACCAATATATGTTTTTATTCGCTTTGCTGATTTTTTCACATG	400
Db	1478 TGACAGAGATTTGTTTAAACAGACCAATATATGTTTTTATTCGCTTTGCTGATTTTTTCACATG	1537
OY	401 TTACCTTTCCAGGTACCAACAGCGGTTACATTGTCTGTGACAGTAGTATACCAAGCTTAC	460
Db	1538 TTACCTTTCCAGGTACCAACAGCGGTTACATTGTCTGTGACAGTAGTATACCAAGCTTAC	1597
OY	461 AGCGGTGTGACGGGATCAGTCGTAACGGGGATGAGATTAATTCGCATTGCTGACTACTT	520
Db	1558 AGCGGTGTGACGGGATCAGTCGTAACGGGGATGAGATTAATTCGCATTGCTGACTACTT	1657
OY	521 CTTATCTGGATTTAATGTGCGATAGTGGAACTCACTAGCAGCATCTGTGGCAAGAGCGA	580
Db	1658 CTTATCTGGATTTAATGTGCGATAGTGGAACTCACTAGCAGCATCTGTGGCAAGAGCGA	1717
OY	581 TGTTAAGGTTTTCTTACTCTGACAGCTGAAGCTTTACGTTTTCCGGAATATACAGAGGGAT	640
Db	1718 TGTTAAGGTTTTCTTACTCTGACAGCTGAAGCTTTACGTTTTCCGGAATATACAGAGGGAT	1777
OY	641 TTCGTACAACACTGGATGATCTCAGTGGGCGTTCTTATGTATGACTCTGAAGATGTTG	700
Db	1778 TTCGTACAACACTGGATGATCTCAGTGGGCGTTCTTATGTATGACTCTGAAGATGTTG	1837
OY	701 ATCTTACATTGAACTGGGGAAAGTTGAGTAGGCTCTGCTGACTATCATGGACAAGACT	760
Db	1838 ATCTTACATTGAACTGGGGAAAGTTGAGTAGGCTCTGCTGACTATCATGGACAAGACT	1897
OY	761 CTGTTTCGTGTGGAAGAATTTCTTTTGGAGCATTTAATGCAATTCTGGGAAAGCGTGGCAT	820
Db	1898 CTGTTTCGTGTGGAAGAATTTCTTTTGGAGCATTTAATGCAATTCTGGGAAAGCGTGGCAT	1957
OY	821 TAAATAGTAATTTGATCATCATGATGATGCGAGTTGCAGAAATGGCATCTGATAGTTTC	880
Db	1958 TAAATAGTAATTTGATCATCATGATGATGCGAGTTGCAGAAATGGCATCTGATAGTTTC	2017
OY	881 CTTCTATGTGTCGGCAGATGGAAGATCCGCTGGATTAACGACAAATAATATTGTTGG	940
Db	2018 CTTCTATGTGTCGGCAGATGGAAGATCCGCTGGATTAACGACAAATAATATTGTTGG	2077
OY	941 ATTCAATCACTCTGGGGCAATTTCTGATGCCAGAACTATTAGCAGTGG 989	
Db	2078 ATTCAATCACTCTGGGGCAATTTCTGATGCCAGAACTATTAGCAGTGG 2126	
RESULT 8		
AAAS1216		
ID	AAAS1216 standard; DNA; 2127 BP.	
XX	AAAS1216;	
AC		
DT	26-SEP-2000 (first entry)	
XX		
DE	MBP-VT-1 subunit A fusion gene.	

XX	VT-1, verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
KM	recombinant production; screening; dairy; anti-bacterial; vaccine;
KM	primer; maltose binding protein; MBP; ds.
XX	
OS	Escherichia coli.
OS	Synthetic.
OS	Chimeric.
XX	
FT	Key
FT	Location/Qualifiers
FT	1. .2127
FT	/*tag= a
FT	/product= "fusion_protein"
FT	1246. .2124
FT	/*tag= b
FT	/product= "Mature_verotoxin-1_subunit_A"
XX	
PN	US6080400-A.
XX	
PD	27-JUN-2000.
XX	
PE	13-MAR-1997; 97US-00816977.
XX	
PR	24-MAR-1995; 95US-00410058.
XX	
PA	(OPHI-) OPHIDIAN PHARM INC.
PI	Williams JA, Byrne LM;
XX	
DR	WPI; 2000-451195/39.
XX	
XX	P-PSDB; AAY95690.
XX	
PT	Bacterial cell for recombinantly expressing bacterial toxins in large
PT	quantities useful for immunization and treatment of bacterial infections,
XX	comprises expression vector encoding bacterial toxin.
XX	
XX	Example 6; Col 101-106; 83pp; English.
XX	
XX	E. coli verotoxin (VT) types 1 and 2 subunit A were cloned into pMal-p2,
CC	designed to allow expression of the native proteins as C-terminal fusions
CC	to a periplasmically-secreted version of maltose binding protein (MBP).
CC	The vector contains an engineered factor Xa cleavage site, which permits
CC	the removal of the affinity tag (i.e. MBP) from the fusion protein after
CC	purification. VT B chains are small proteins (approximately 8 kDa), so
CC	use of a small affinity tag was preferred (i.e. polyhistidine). A
CC	polyhistidine affinity tag facilitates single step affinity purification
CC	of subunits from periplasmic extracts. However, due to poor recovery of
CC	his-tagged VT-1 A and VT-2 A chains, expression of MBP fused subunits was
CC	undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced
CC	promoter control is necessary to permit cell viability. Bacterial host
CC	cells expressing a recombinant expression vector encoding a polyhistidine
CC	affinity tag and a portion of the VT-2 B chain are claimed. The vector is
CC	chosen from PET24hisVT2BL+, PET24hisVT2BL- and PET24VT2B, where "L."
CC	indicates that the vector encodes the preprotein form of the protein and
CC	"L-" indicates that the vector encodes the mature form of the protein.
CC	The bacterial cell is capable of expressing large quantities (40 mg/l) of
CC	VT-2B. The toxins are useful for immunizing non-mammals and for detecting
CC	bacterial toxins in environmental samples including soil, water,
CC	industrial samples, biological samples and samples obtained from food and
CC	dairy processing instruments
XX	
SO	Sequence 2127 BP; 592 A; 463 C; 546 G; 526 T; 0 U; 0 Other;
XX	
Query Match	58.4%; Score 879.4; DB 3; Length 2127;
Best Local Similarity	99.3%; Pred. No. 4.7e-253;
Matches 883; Conservative	0; Mismatches 6; Indels 0; Gaps 0;
0Y	101 CAGATTCGAAGCAATTACCTTAGACTTCTGCAGCTGCACAAGACGATATAGATTGCGTGA 160
DB	1238 CAGAAITTCAGCAATTATTAACCTTAGACTTCTGCAGCTGCACAAGACGATATATGATTGCGTGA 1299
0Y	161 ATGTCATTGCGCTCTGCACATAGTACTGTCATTACAGACTATTTCAATCAGAGAGTACGTTT 220


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Db 1538 TTACCTTTCCAGGTACCAAGCGGTTACATTGTCTGTGACAGTAGCTAATACCAAGTTAC 1597
Qy 461 AGCGGTGGCGAGGATCATGCTGTACGGGATGCGAGATTAATCCGATTCGTTGACTCTT 520
Db 1598 AGCGGTGGCGAGGATCATGCTGTACGGGATGCGAGATTAATCCGATTCGTTGACTCTT 1657
Qy 521 CTTATCTGGATTATATGTCGATAGTGGAACTCCTGACAGCAGTCTGTGGCAAGAGCA 580
Db 1658 CTTATCTGGATTATATGTCGATAGTGGAACTCCTGACAGCAGTCTGTGGCAAGAGCA 1717
Qy 581 TGTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGGCAATACAGAGGGAT 640
Db 1718 TGTACGGTTTGTACTGTGACAGCTGAAGCTTTACGTTTTCGGCAATACAGAGGGAT 1777
Qy 641 TTCCGACAACTGATGATCTCAGTGGCGCTTATATGATGATGCTGATGAGATGTTG 700
Db 1778 TTCCGACAACTGATGATCTCAGTGGCGCTTATATGATGATGCTGATGAGATGTTG 1837
Qy 701 ATCTTACATTGAACCTGGGAAAGTTGAGTAGCGTCTGCTGACTATCATGAGACAACT 760
Db 1838 ATCTTACATTGAACCTGGGAAAGTTGAGTAGCGTCTGCTGACTATCATGAGACAACT 1897
Qy 761 CTGTTGCTGTAGGAAGAAATTTCTTTTGAAGCATTATGCAATTTCTGGAAACCGTGCAT 820
Db 1898 CTGTTGCTGTAGGAAGAAATTTCTTTTGAAGCATTATGCAATTTCTGGAAACCGTGCAT 1957
Qy 821 TAATACGTGAATGTGATCATCATGATGCGGAGTTGCGGAGATGAGCATCTGTAGAGTTTC 880
Db 1958 TAATACGTGAATGTGATCATCATGATGCGGAGTTGCGGAGATGAGCATCTGTAGAGTTTC 2017
Qy 881 CTTCTATGTGTGTCGCGAGATGGAAGAGTCCGTGGGATTAACGCAATTAATAATTTGTGGG 940
Db 2018 CTTCTATGTGTGTCGCGAGATGGAAGAGTCCGTGGGATTAACGCAATTAATAATTTGTGGG 2077
Qy 941 ATTCAATCCACTCTGGGGGCAATTTCTGATGCCGACAGACTATTAGCAGTGG 989
Db 2078 ATTCAATCCACTCTGGGGGCAATTTCTGATGCCGACAGACTATTAGCAGTGG 2126

RESULT 10
ADL25577
ID ADL25577 standard; DNA; 1227 BP.
XX
AC ADL25577;
XX
DT 20-MAY-2004 (first entry)
XX
DE S. sonnei shiga toxin gene stx-sonnei.
XX
KM Shiga toxin; ds; gene; fluorescence resonance energy transfer; FRET;
XX
KW gastrointestinal disease; dysentery.
XX
OS Shigella sonnei.
XX
XX US2003215814-A1.
XX
XX 20-NOV-2003.
XX
XX 17-MAY-2002; 2002US-00150792.
XX
XX 17-MAY-2002; 2002US-00150792.
XX
XX (COCK/) COCKERILL F R.
XX
XX (ROSE/) ROSENBLATT J E.
XX
XX (SLOAN/) SLOAN L.
XX
XX (UHLJ/) UHL J R.
XX
XX Cockerill FR, Rosenblatt JE, Sloan L, Uhl JR;
XX
XX WPI; 2003-902026/82.
XX
XX Detecting presence or absence of Shiga toxin producing organisms in
XX biological sample, by amplifying nucleic acid encoding Shiga toxin with
PT

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PT pair of stx1 primers and detecting fluorescence resonance energy
PT transfer.
XX
XX Example 2; Fig 1; 24pp: English.
XX
XX The invention relates to detecting the presence or absence of Shiga toxin
CC or Shiga-like toxin producing organisms in a biological sample involving
CC amplifying nucleic acid encoding Shiga toxin with a pair of stx1 primers,
CC detecting the amplified product with labelled stx1 probes, and detecting
CC the presence or absence of fluorescence resonance energy transfer (FRET).
CC Also included is an article of manufacture comprising the stx1 primers
CC and probes and a donor fluorescent moiety and corresponding fluorescent
CC moiety or a pair of stx2 primers, a pair of stx2 probes and a donor
CC fluorescent moiety and corresponding fluorescent moiety. The method is
CC useful for detecting the presence or absence of one or more Shiga toxin
CC or Shiga-like toxin producing organisms e.g. Escherichia coli (especially
CC gastrointestinal disease causing strains) and Shigella (causative agent
CC of dysentery) in a biological sample which is a stool sample or body
CC fluids from an individual. The method is rapid and specific in detecting
CC the Shiga toxin from biological samples. The present sequence is a
CC bacterial shiga toxin or shiga-like toxin gene used to design the primers
CC and probes of the invention.
XX
XX Sequence 1227 BP; 335 A; 203 C; 297 G; 392 T; 0 U; 0 Other;
SQ
Query Match 58.3%; Score 879; DB 11; Length 1227;
Best Local Similarity 99.4%; Pred. No. 4.6e-253;
Matches 882; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 103 GATCTGAAGAAATTTACCTTATGACTCTGACCTGCAAGAGCGTATGATGCTGAT 162
Db 61 GTTCCGAAGGAATTTACCTTATGACTCTGACCTGCAAGAGCGTATGATGCTGAT 120
Qy 163 GTCAATGCGCTCTGCAATAGTACTCCATTACAGACTATTTTATCAGAGAGTACGTCCTTTA 222
Db 121 GTCAATGCGCTCTGCAATAGTACTCCATTACAGACTATTTTATCAGAGAGTACGTCCTTTA 180
Qy 223 CTGATGATTGATGTGCGACAGGGGATTAATTTGTTTGGCAGTTGATGTCAGAGGGATAGAT 282
Db 181 CTGATGATTGATGTGCGACAGGGGATTAATTTGTTTGGCAGTTGATGTCAGAGGGATAGAT 240
Qy 283 CCAGAGGAAGGGCGGTTTAATATCTACGGCTTATGTTGTAAGCAATTAATTTATATG 342
Db 241 CCAGAGGAAGGGCGGTTTAATATCTACGGCTTATGTTGTAAGCAATTAATTTATATG 300
Qy 343 ACAGGATTTGTTAACAGACAAATATGTTTTTATATGCGTTGCTGATTTTTCACATGTT 402
Db 301 ACAGGATTTGTTAACAGACAAATATGTTTTTATATGCGTTGCTGATTTTTCACATGTT 360
Qy 403 ACCTTTCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTACTATACCAAGCTTACAG 462
Db 361 ACCTTTCCAGGTACAAACAGCGGTTACATTGTCTGTGACAGTACTATACCAAGCTTACAG 420
Qy 463 CGTGTGGAGGAGTACAGTCGTACGGGGATGCGAGATTAATGCGCATTCGTTGACTACTTCT 522
Db 421 CGTGTGGAGGAGTACAGTCGTACGGGGATGCGAGATTAATGCGCATTCGTTGACTACTTCT 480
Qy 523 TATCTGATTTTAATGTCGATAGTGAACCTCACTGACGAGCTGTGGCAAGAGCGATG 582
Db 481 TATCTGATTTTAATGTCGATAGTGAACCTCACTGACGAGCTGTGGCAAGAGCGATG 540
Qy 583 TTACGGTTTGTACTGTGACAGCTGAAGCTTTAGCTTTTCCGCAATACAGAGGGGATTT 642
Db 541 TTACGGTTTGTACTGTGACAGCTGAAGCTTTAGCTTTTCCGCAATACAGAGGGGATTT 600
Qy 643 CGTACAACTGATGATCTCAGTGGGCGTTCTTATGTAATGACTGTGAAGATGTTGAT 702
Db 601 CGTACAACTGATGATCTCAGTGGGCGTTCTTATGTAATGACTGTGAAGATGTTGAT 660
Qy 703 CTTACATTGAACCTGGGGAAGGTTGAGTAGCGTCTGCTGACTATCATGACAAAGACTCT 762
Db 661 CTTACATTGAACCTGGGGAAGGTTGAGTAGCGTCTGCTGACTATCATGACAAAGACTCT 720

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OY 763 GTTCGTGTAGAGAAATTTCTTTGGAGACATTAATGCAATTCCTGGAGACGTGCATTA 822
DB 721 GTTCGTGTAGAGAAATTTCTTTGGAGACATTAATGCAATTCCTGGAGACGTGCATTA 780
OY 823 ATACTGAATTTGATCATCATCATGATCCGAGTTGCCAGATGGCATCTGATGATTTCT 882
DB 781 ATACTGAATTTGATCATCATCATGATCCGAGTTGCCAGATGGCATCTGATGATTTCT 840
OY 883 TCTATGTGTCGGCAGATGAGAGATCCGTGGATTACGACATTAATAATATTGGAGAT 942
DB 841 TCTATGTGTCGGCAGATGAGAGATCCGTGGATTACGACATTAATAATATTGGAGAT 900
OY 943 TCATCCACTCTGCGGCAATTCGTATGTCGAGAACTATTAGCAGTGG 989
DB 901 TCATCCACTCTGCGGCAATTCGTATGTCGAGAACTATTAGCAGTGG 947

RESULT 11
ID AEE48613 standard; DNA; 1227 BP.
XX AEE48613;
AC AEE48613;
XX
XX 23-FEB-2006 (first entry)
XX
XX Shigella sonnei shiga-like toxin gene stx-sonnei.
XX
XX Microorganism detection; Shiga-like toxin; gene; ds.
XX
XX Shigella sonnei.
XX
XX US2005282194-A1.
XX
XX 22-DEC-2005.
XX
XX 29-APR-2005; 2005US-00117858.
XX
XX 17-MAY-2002; 2002US-00150792.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX Cockerill FR, Rosenblatt JE, Sloan LM, Uhl JR;
XX
XX WPI; 2006-046433/05.
XX
XX
XX Detecting Shiga-like toxin-producing organisms in sample, by detecting
XX fluorescence resonance energy transfer between probes after amplifying
XX PT and hybridizing toxin nucleic acid in sample with toxin specific primers
XX and labeled probes.
XX
XX Example 2; Fig 1; 25pp; English.
XX
XX The present invention relates to a method (M1) for detecting the presence
XX CC or absence of Shiga toxin (stx) - or Shiga-like toxin (stx1/stx2) -
XX CC producing organisms in sample. The method comprises performing cycling
XX CC step comprising amplifying and hybridizing steps, using sample, primers
XX CC and labeled probes for nucleic acid molecule encoding the toxin, and
XX CC detecting presence of fluorescence resonance energy transfer (FRET)
XX CC between donor fluorescent moiety of first probe and acceptor fluorescent
XX CC moiety of second probe. The present sequence is a Shiga-like toxin which
XX CC was used in a sequence homology alignment to illustrate the invention.
XX
XX Sequence 1227 BP; 335 A; 203 C; 297 G; 392 T; 0 U; 0 Other;
SQ

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DB 121 GTTCATTCCTCGCAATAGTAATCTCCATTACAGATTAATTTATCATCGAGGATGCTTTA 180
OY 223 CTGATGATTTGATAGTGGCAACAGGGATTAATTTGTTTCAGTTGATGTCAGAGGGATAGAT 282
DB 181 CTGATGATTTGATAGTGGCAACAGGGATTAATTTGTTTCAGTTGATGTCAGAGGGATAGAT 240
OY 283 CCAGAGGAAGGCGGTTTAATTAATCTACCGCTTAATTTGTAACGAATTAATTAATGTCG 342
DB 241 CCAGAGGAAGGCGGTTTAATTAATCTACCGCTTAATTTGTAACGAATTAATTAATGTCG 300
OY 343 AAGAGATTTGTTTAACAGAGCAAAATTAATGTTTATTCCTTTCAGATTTTTCACATGTT 402
DB 301 AAGAGATTTGTTTAACAGAGCAAAATTAATGTTTATTCCTTTCAGATTTTTCACATGTT 360
OY 403 ACCTTTCCAGTACAAACAGCGGTTACATTTGTCGTGACAGTAGCTATTAACACGTTACG 462
DB 361 ACCTTTCCAGTACAAACAGCGGTTACATTTGTCGTGACAGTAGCTATTAACACGTTACG 420
OY 463 CGTGTGACAGGATCAGTGTGACGCGGATGACAGATTAATGCCATTGCTTGAATCTTCT 522
DB 421 CGTGTGACAGGATCAGTGTGACGCGGATGACAGATTAATGCCATTGCTTGAATCTTCT 480
OY 523 TATCTGATTTAATGTCGATAGTGAACCTCAGACGAGCTGTCGAGCAAGAGCATG 582
DB 481 TATCTGATTTAATGTCGATAGTGAACCTCAGACGAGCTGTCGAGCAAGAGCATG 540
OY 583 TTACGGTTTGTACTGTCGACACCTGAAGCTTTTACGTTTTCGCAAAATACAGAGGGATTT 642
DB 541 TTACGGTTTGTACTGTCGACACCTGAAGCTTTTACGTTTTCGCAAAATACAGAGGGATTT 600
OY 643 CGTACAAACCTGATGATCTCAGTGGCGGTTTATGATTAATACCTGCTGAAGATGTTAT 702
DB 601 CGTACAAACCTGATGATCTCAGTGGCGGTTTATGATTAATACCTGCTGAAGATGTTAT 660
OY 703 CTTACATTAACCTGGGGAAGGTTGATGATGCTCCGCTGACATCATGAGCAAGACTCT 762
DB 661 CTTACATTAACCTGGGGAAGGTTGATGATGCTCCGCTGACATCATGAGCAAGACTCT 720
OY 763 GTTCGTGTAGAGAAATTTCTTTGGAGACATTAATGCAATTCCTGGAGACGTGCATTA 822
DB 721 GTTCGTGTAGAGAAATTTCTTTGGAGACATTAATGCAATTCCTGGAGACGTGCATTA 780
OY 823 ATACTGAATTTGATCATCATCATGATCCGAGTTGCCAGATGGCATCTGATGATTTCT 882
DB 781 ATACTGAATTTGATCATCATCATGATCCGAGTTGCCAGATGGCATCTGATGATTTCT 840
OY 883 TCTATGTGTCGGCAGATGAGAGATCCGTGGATTACGACATTAATAATATTGGAGAT 942
DB 841 TCTATGTGTCGGCAGATGAGAGATCCGTGGATTACGACATTAATAATATTGGAGAT 900
OY 943 TCATCCACTCTGCGGCAATTCGTATGTCGAGAACTATTAGCAGTGG 989
DB 901 TCATCCACTCTGCGGCAATTCGTATGTCGAGAACTATTAGCAGTGG 947

RESULT 12
ADL25575
ID ADL25575 standard; DNA; 1227 BP.
XX ADL25575;
AC ADL25575;
XX
XX 20-MAY-2004 (first entry)
XX
XX Bacteriophage h30 shiga toxin gene stx1.
XX
XX Shiga toxin; ds; gene; fluorescence resonance energy transfer; FRET;
XX km gastrointestinal disease; dysentery.
XX
XX Bacteriophage h30.
XX
XX US2003215814-A1.
XX

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PD 20-NOV-2003.
 XX 17-MAY-2002; 2002US-00150792.
 XX 17-MAY-2002; 2002US-00150792.
 XX 17-MAY-2002; 2002US-00150792.
 XX (COCK/) COCKERILL F R.
 PA (ROSE/) ROSENBLATT J E.
 PA (SLOAN/) SLOAN L.
 PA (UHLJ/) UHL J R.
 XX Cockerill FR, Rosenblatt JE, Sloan L, Uhl JR;
 PI WPI; 2003-902026/82.
 DR
 XX
 PT Detecting presence or absence of Shiga toxin producing organisms in
 PT biological sample, by amplifying nucleic acid encoding Shiga toxin with
 PT pair of stx1 primers and detecting fluorescent resonance energy
 PT transfer.
 PT
 XX
 PS Example 2; Fig 1; 24pp; English.
 XX
 CC The invention relates to detecting the presence or absence of Shiga toxin
 CC or Shiga-like toxin producing organisms in a biological sample involving
 CC amplifying nucleic acid encoding Shiga toxin with a pair of stx1 primers,
 CC detecting the amplified product with labelled stx1 probes, and detecting
 CC the presence or absence of fluorescence resonance energy transfer (FRET).
 CC Also included is an article of manufacture comprising the stx1 primers
 CC and probes and a donor fluorescent moiety and corresponding fluorescent
 CC moiety or a pair of stx2 primers, a pair of stx2 probes and a donor
 CC fluorescent moiety and corresponding fluorescent moiety. The method is
 CC useful for detecting the presence or absence of one or more Shiga toxin
 CC or Shiga-like toxin producing organism e.g. Escherichia coli (especially
 CC gastrointestinal disease causing strains) and Shigella (causative agent
 CC of dysentery) in a biological sample which is a stool sample or body
 CC fluids from an individual. The method is rapid and specific in detecting
 CC the Shiga toxin from biological samples. The present sequence is a
 CC bacterial Shiga toxin or Shiga-like toxin gene used to design the primers
 CC and probes of the invention.
 CC
 XX
 SQ Sequence 1227 BP; 334 A; 205 C; 298 G; 390 T; 0 U; 0 Other;
 Query Match 58.3%; Score 878.8; DB 11; Length 1227;
 Best Local Similarity 99.8%; Pred. No. 5.2e-253;
 Matches 880; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 108 GAAGGAATTTACCTAGACTCTCGACGCAAGAGCGATGATGAGTTCGCTGAAATGTCAT 167
 DB 66 GAAGGAATTTACCTAGACTCTCGACGCAAGAGCGATGATGAGTTCGCTGAAATGTCAT 125
 QY 168 TCGCTCTGCAATAGTAGTCTCCATTACAGACTATTTTCATCAGAGAGTACGCTTTACTGAT 227
 DB 126 TCGCTCTGCAATAGTAGTCTCCATTACAGACTATTTTCATCAGAGAGTACGCTTTACTGAT 185
 QY 228 GATTGATAGTGGCAGAGGGGATTAATTTGTTGCAAGTATGTCAGAGGATGATCCGA 287
 DB 186 GATTGATAGTGGCAGAGGGGATTAATTTGTTGCAAGTATGTCAGAGGATGATCCGA 245
 QY 288 GGAAGGGGCGTTTAATATATCTACGCGCTATTGTTGAAGCAATATATTTATGTCAGAGG 347
 DB 246 GGAAGGGGCGTTTAATATATCTACGCGCTATTGTTGAAGCAATATATTTATGTCAGAGG 305
 QY 348 ATTGTTAACAGAGCAAAATATGTTTTTATGCTGTTGCTGATTTTTCACATGTTACCTT 407
 DB 306 ATTGTTAACAGAGCAAAATATGTTTTTATGCTGTTGCTGATTTTTCACATGTTACCTT 365
 QY 408 TTCAGGTACAGAGCGGTATCTTCTGTCGACAGTATGATATACAGAGTTCAGAGCGTGT 467
 DB 366 TTCAGGTACAGAGCGGTATCTTCTGTCGACAGTATGATATACAGAGTTCAGAGCGTGT 425
 QY 468 TGCAGAGGATCTGATCTGACGGGATGCAGATTAATGCGCATTCGTTGACATCTTATATCT 527
 DB 426 TGCAGAGGATCTGATCTGACGGGATGCAGATTAATGCGCATTCGTTGACATCTTATATCT 485

QY 528 GGATTTATGTCGCATAGTAGTGAACCTTCACCTAGCAGAGTCTGTGGCAAGAGCGATGTTACG 587
 DB 486 GGATTTATGTCGCATAGTAGTGAACCTTCACCTAGCAGAGTCTGTGGCAAGAGCGATGTTACG 545
 QY 588 GTTTGTTACTGTGACACGCTGAAGCTTTAGCTTTTGGCAATATACAGAGGGGATTTGCTAC 647
 DB 546 GTTTGTTACTGTGACACGCTGAAGCTTTAGCTTTTGGCAATATACAGAGGGGATTTGCTAC 605
 QY 648 AACACGTGATGATCTGACGCGGGGCTTCTTATGTAATGACCTGGAAGATGTTGATCTTAC 707
 DB 606 AACACGTGATGATCTGACGCGGGGCTTCTTATGTAATGACCTGGAAGATGTTGATCTTAC 665
 QY 708 ATTGAACGTGGGAAGGTTGAGTAGCGCTCTGCTGACTATATGACAGCAAGACTCTGTTG 767
 DB 666 ATTGAACGTGGGAAGGTTGAGTAGCGCTCTGCTGACTATATGACAGCAAGACTCTGTTG 725
 QY 768 TGTGGAAGAATTTCTTTTGGGAAGCATTAATGCAATTTCTGGGAAGCTGGCATTAATACT 827
 DB 726 TGTGGAAGAATTTCTTTTGGGAAGCATTAATGCAATTTCTGGGAAGCTGGCATTAATACT 785
 QY 828 GAATTCATCATCATCATCATCGAGTTCGAGATGCGAGATGCGATGATGATGTTCTCTCAT 887
 DB 786 GAATTCATCATCATCATCATCGAGTTCGAGATGCGAGATGCGATGATGATGATGTTCTCTCAT 845
 QY 888 GTGTCCGCGAGATGGAAGAGTCCGTGGATTAACGACAAATTAATTTGTGGATTCATC 947
 DB 846 GTGTCCGCGAGATGGAAGAGTCCGTGGATTAACGACAAATTAATTTGTGGATTCATC 905
 QY 948 CACTCTGGGGCAATTTGATGCGGCAACTATTTAGCAGATG 989
 DB 906 CACTCTGGGGCAATTTGATGCGGCAACTATTTAGCAGATG 947
 RESULT 13
 AEB48611
 ID AEB48611 standard; DNA; 1227 BP.
 XX
 AC AEB48611;
 XX
 DT 23-FEB-2006 (first entry)
 XX
 DE Bacteriophage h30 shiga-like toxin gene stx1.
 XX
 KW Microorganism detection; Shiga-like toxin; gene; ds.
 XX
 OS Bacteriophage h30.
 XX
 FN US2005282194-A1.
 XX
 XX 22-DEC-2005.
 PD
 PF 29-APR-2005; 2005US-00117858.
 XX
 XX 17-MAY-2002; 2002US-00150792.
 XX
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 PI Cockerill FR, Rosenblatt JE, Sloan LM, Uhl JR;
 DR WPI; 2006-046433/05.
 XX
 XX
 PT Detecting Shiga-like toxin-producing organisms in sample, by detecting
 PT fluorescence resonance energy transfer between probes after amplifying
 PT and hybridizing toxin nucleic acid in sample with toxin specific primers
 PT and labeled probes.
 XX
 PS Example 2; Fig 1; 25pp; English.
 XX
 CC The present invention relates to a method (M1) for detecting the presence
 CC or absence of Shiga toxin (stx)- or Shiga-like toxin (stx1/stx2) -
 CC producing organisms in sample. The method comprises performing cycling
 CC step comprising amplifying and hybridizing steps, using sample, primers

CC and labeled probes for nucleic acid molecule encoding the toxin, and
 CC detecting presence of fluorescence resonance energy transfer (FRET)
 CC between donor fluorescent moiety of first probe and acceptor fluorescent
 CC moiety of second probe. The present sequence is a Shiga-like toxin which
 CC was used in a sequence homology alignment to illustrate the invention.

XX
 XX
 SQ Sequence 1227 BP; 334 A; 205 C; 298 G; 390 T; 0 U; 0 Other;

Query Match 58.3%; Score 878.8; DB 15; Length 1227;
 Best Local Similarity 99.8%; Pred. No. 5.2e-253;
 Matches 880; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACCTTAGACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 167
 DB 66 GAAGGAATTTACCTTAGACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 125
 QY 168 TCGCTCTGCAATAGTACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 227
 DB 126 TCGCTCTGCAATAGTACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 185
 QY 228 GATTGATAGTGGACAGGGGATTAATTTGTTGCAAGTATGATGCTGTAATGCAT 287
 DB 186 GATTGATAGTGGCTCAGGGGATTAATTTGTTGCAAGTATGATGCTGTAATGCAT 245
 QY 288 GGAAGGCGGTTTAATATCTACCGCTTATTTGGAACGAATATTTATATGTCAGG 347
 DB 246 GGAAGGCGGTTTAATATCTACCGCTTATTTGGAACGAATATTTATATGTCAGG 305
 QY 348 ATTTGTTAACAGCAAAATATGTTTTTATCGCTTGTGATGTTTTTACATGTTACTT 407
 DB 306 ATTTGTTAACAGCAAAATATGTTTTTATCGCTTGTGATGTTTTTACATGTTACTT 365
 QY 408 TCCAGGTACAACAGCGGTTTACCTGTTCTGTCAGTACAGTACGATACCAAGCTTACAGGCTG 467
 DB 366 TCCAGGTACAACAGCGGTTTACCTGTTCTGTCAGTACAGTACGATACCAAGCTG 425
 QY 426 TGACAGGATCAGTCTGTCAGGGGATGACATTAATTCGCTGTTGACTCTTCTTAATCT 485
 DB 528 GGAATTTAATGTCGATGTCGAACTCTACGACGCACTGTCGCAAGAGCGATGTTACG 587
 QY 486 GGAATTTAATGTCGATGTCGAACTCTACGACGCACTGTCGCAAGAGCGATGTTACG 545
 QY 588 GTTTGTTACTGTGACAGCTTACGTTTTCGCAAAATACAGAGGGGATTTCTGTAC 647
 DB 546 GTTTGTTACTGTGACAGCTTACGTTTTCGCAAAATACAGAGGGGATTTCTGTAC 605
 QY 648 AACACTGATGATCTCAGTGGCGCTTTATATGATGATGCTGAGATGTTGATCTTAC 707
 DB 606 AACACTGATGATCTCAGTGGCGCTTTATATGATGATGCTGAGATGTTGATCTTAC 665
 QY 708 ATTGAATCTGGGAAGTGTAGTACGCTTCTGCTGATATCAGCAAAAGCTGTTGCG 767
 DB 666 ATTGAATCTGGGAAGTGTAGTACGCTTCTGCTGATATCAGCAAAAGCTGTTGCG 725
 QY 768 TGTAGAAGAATTTCTTTTGAAGCATTAATGCAATTTCTGGAAGCGCTGCAATTAATCT 827
 DB 726 TGTAGAAGAATTTCTTTTGAAGCATTAATGCAATTTCTGGAAGCGCTGCAATTAATCT 785
 QY 828 GAATTTGATCATCATGATCGGAGTGTGCGAAGTGGCATTCGATGATGTTCTCTTAT 887
 DB 786 GAATTTGATCATCATGATCGGAGTGTGCGAAGTGGCATTCGATGATGTTCTCTTAT 845
 QY 888 GTGTCCGCGAGATGGAAGAGTCCGTGGGATTAACGCAAAATATTTGTTGGGATTCATC 947
 DB 846 GTGTCCGCGAGATGGAAGAGTCCGTGGGATTAACGCAAAATATTTGTTGGGATTCATC 905
 QY 948 CACTCTGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 989
 DB 906 CACTCTGGGGCAATTTCTGATGCGCAGAACTATTAGCAGTGG 947

RESULT 14
 AAV11400
 ID AAV11400 standard; DNA; 1389 BP.
 XX
 AC AAV11400;
 XX
 DT 18-AUG-1998 (first entry)
 XX
 DE Shiga toxin type 1 gene.
 DE
 KW Histone-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx;
 KW haemorrhagic colitis; haemolytic uremic syndrome; ss.
 XX
 OS Shigella dysenteriae.
 XX
 FH Key location/Qualifiers
 FT CDS 229..1110
 FT /tag= a
 FT /product= "Stx1 A subunit"
 FT /note= "No start codon given"
 FT CDS 1120..1389
 FT /tag= b
 FT /product= "Stx1 B subunit"
 FT
 PN W09811229-A2.
 PN
 PD 19-MAR-1998.
 PD
 XX
 PF 09-SEP-1997; 97WO-US015836.
 PF
 XX
 PR 10-SEP-1996; 96US-0025637P.
 PR
 XX
 PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 PA
 PI Obrien AD, Schmitz CK;
 PI
 DR WPI; 1998-207390/18.
 DR
 DR P-PSDB; AAM58827, AAM58828.
 DR
 XX
 PT Purification and isolation of histidine-tagged Shiga toxins - useful in
 PT vaccines against haemorrhagic colitis and haemolytic uremic syndrome.
 PT
 XX
 PS Claim 1; Fig 4; 47p; English.
 PS
 XX
 CC The Shiga toxin (Stx) genes (AAV11400-V11401) both encode two separate
 CC peptides. The peptides are histidine-tagged to simplify and expedite
 CC purification. Non toxic Shiga toxoids. Fusion proteins of His-tagged
 CC Shiga toxins/toxoids and antibodies can be used in the treatment.
 CC diagnosis or prevention of infections mediated by toxins of the Stx
 CC family. These are associated with haemorrhagic colitis and the life-
 CC threatening sequelae, haemolytic uremic syndrome. Shiga antibodies are
 CC also useful for the treatment, diagnosis and prevention of disease and
 CC infections by pathogenic Escherichia coli
 CC
 XX
 SQ Sequence 1389 BP; 373 A; 232 C; 337 G; 447 T; 0 U; 0 Other;

Query Match 58.3%; Score 878.8; DB 2; Length 1389;
 Best Local Similarity 99.8%; Pred. No. 5.6e-253;
 Matches 880; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 108 GAAGGAATTTACCTTAGACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 167
 DB 228 GAAGGAATTTACCTTAGACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 287
 QY 168 TCGCTCTGCAATAGTACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 227
 DB 288 TCGCTCTGCAATAGTACTTCTGACCTGCAAAAGCTATGATGCTGTAATGCAT 347
 QY 228 GATTGATAGTGGACAGGGGATTAATTTGTTGCAAGTATGATGCTGTAATGCAT 287
 DB 348 GATTGATAGTGGCTCAGGGGATTAATTTGTTGCAAGTATGATGCTGTAATGCAT 407
 QY 288 GGAAGGCGGTTTAATATCTACCGCTTATTTGGAACGAATATTTATATGTCAGG 347

Dd		408	GGAAGGGCGGTTTAATATCTACGCCCTATTGTTCAGAAATAATATATATGTGCACGG	467
Oy		348	ATTGTGTAACAGACAATAAATGTTTTTATTCGCTTGCTGATYTTTTTCAGATGTTACC	407
Dd		468	ATTGTGTAACAGACAATAAATGTTTTTATTCGCTTGCTGATYTTTTTCAGATGTTACC	527
Oy		408	TCCAGGTCAACAACGGGCTTACTAGTCTCNGTGACAGTAGCATATACAGTACAGCCGGT	467
Dd		528	TCCAGGTCAACAACGGGCTTACTAGTCTCNGTGACAGTAGCATATACAGTACAGCCGGT	587
Oy		468	TGCAGGAGTCAAGTGTGACGGGATGCAGATTAATGCCATTCGTTGACTACTYCTTACT	527
Dd		588	TGCAGGAGTCAAGTGTGACGGGATGCAGATTAATGCCATTCGTTGACTACTYCTTACT	647
Oy		528	GGATTTAATGTTCGATATGTGAACTCACTGACGCAAGTCTGTGGCAAGAGATGTTACG	587
Dd		648	GGATTTAATGTTCGATATGTGAACTCACTGACGCAAGTCTGTGGCAAGAGATGTTACG	707
Oy		588	GTTTGTACTGTGACAGCTGAAGCTTTACGTTTTGCGCAAAATPACAGGGGATTTGCTAC	647
Dd		708	GTTTGTACTGTGACAGCTGAAGCTTTACGTTTTGCGCAAAATPACAGGGGATTTGCTAC	767
Oy		648	AACACTGATATCTCAGTGTGGCGCTTCTTATGTATAATGATCTGCTGAAGATGTTGATCTTAC	707
Dd		768	AACACTGATATCTCAGTGTGGCGCTTCTTATGTATAATGATCTGCTGAAGATGTTGATCTTAC	827
Oy		708	ATTGAACCTGGGGAGGTGAGTAGCGTCCTGCTGATCATATGACAGAAGCTCGTTACG	767
Dd		828	ATTGAACCTGGGGAGGTGAGTAGCGTCCTGCTGATCATATGAGACAAGACTCTGTTTCG	887
Oy		768	TGTAGGAAGAATTTCTTTTGGAGCATTAAATGCAATTCGCGGAACCGTGGCATTAATACT	827
Dd		888	TGTAGGAAGAATTTCTTTTGGAGCATTAAATGCAATTCGCGGAACCGTGGCATTAATACT	947
Oy		828	GAATGTATATCATCATGATCGCGAGTGTGCCAGAAATGGCATCTGATGAGTTTCTTCTAT	887
Dd		948	GAATGTATATCATCATGATCGCGAGTGTGCCAGAAATGGCATCTGATGAGTTTCTTCTAT	1007
Oy		888	GTGTCCGCGCAGATGGAAGAGTCCGTGGGATTACGACAAATAAATATTGTGGATTATC	947
Dd		1008	GTGTCCGCGCAGATGGAAGAGTCCGTGGGATTACGACAAATAAATATTGTGGATTATC	1067
Oy		948	CACCTCTGGGGGCATTTCTGATGCGCAGAACTATTAGCACGTGG	989
Dd		1068	CACCTCTGGGGGCATTTCTGATGCGCAGAACTATTAGCACGTGG	1109
RESULT 15				
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XX	ID	AAT42673		
XX	AC	AAT42673;		
XX	DT	26-FEB-1997	(first entry)	
XX		Flag tag/VTI A subunit fusion construct.		
XX				
KW		Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine;		
XX		haemolytic uremic syndrome; detection; ss.		
OS		Escherichia coli.		
XX				
FX	Key	Location/Qualifiers		
FT	CDS	1..980		
FT		/tag= a		
FT		/product= "Flag/VTI fusion protein"		
XX	PN	WO9630043-A1.		
XX	PD	03-OCT-1996.		
PF		25-MAR-1996; 96WO-US004093.		

Query Match	Best Local Similarity	Score	DB 2	Length	980;
Matches	894;	Conservative	0;	Mismatches	26;
				Indels	0;
				Gaps	0
Sequence	980 BP;	258 A;	177 C;	250 G;	295 T; 0 U; 0 Other;
Query Match	58.3%;	Score	878.4;	DB 2	Length
Best Local Similarity	97.2%;	Pred.	No. 6.1e-253;		
Matches	894;	Conservative	0;	Mismatches	26;
				Indels	0;
				Gaps	0
Sequence	980 BP;	258 A;	177 C;	250 G;	295 T; 0 U; 0 Other;
Query Match	58.3%;	Score	878.4;	DB 2	Length
Best Local Similarity	97.2%;	Pred.	No. 6.1e-253;		
Matches	894;	Conservative	0;	Mismatches	26;
				Indels	0;
				Gaps	0
Sequence	980 BP;	258 A;	177 C;	250 G;	295 T; 0 U; 0 Other;
Query Match	58.3%;	Score	878.4;	DB 2	Length
Best Local Similarity	97.2%;	Pred.	No. 6.1e-253;		
Matches	894;	Conservative	0;	Mismatches	26;
				Indels	0;
				Gaps	0
Sequence	980 BP;	258 A;	177 C;	250 G;	295 T; 0 U; 0 Other;
Query Match	58.3%;	Score	878.4;	DB 2	Length
Best Local Similarity	97.2%;	Pred.	No. 6.1e-253;		
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				Indels	0;
				Gaps	0
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				Indels	0;
				Gaps	0
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Best Local Similarity	97.2%;	Pred.	No. 6.1e-253;		
Matches	894;	Conservative	0;	Mismatches	26;
				Indels	0;
				Gaps	0
Sequence	980 BP;	258 A;	177 C;	250 G;	295 T; 0 U; 0 Other;
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				Indels	0;
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				Indels	0;
				Gaps	0
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Query Match	58.3%;	Score	878.4;	DB 2	Length
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				Indels	0;
				Gaps	0
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Query Match	58.3%;	Score	878.4;	DB 2	Length
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QY      970 CGCAGAACTATTAGCAGTGG 989
Db      961 CGCAGAACTATTAGCAGTGG 980
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job time : 1025 secs

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:31:07 ; Search time 1144 Seconds
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	875.8	58.1	948	US-11-177-646-413	Sequence 413, Appl
2	498.4	33.1	502	US-11-136-524-93	Sequence 93, Appl
3	498	33.0	576	US-11-021-541-2	Sequence 2, Appl
4	498	33.0	576	US-11-422-932-3	Sequence 3, Appl
5	498	33.0	576	US-11-422-947-3	Sequence 3, Appl
6	498	33.0	576	US-11-423-006-3	Sequence 3, Appl
7	498	33.0	576	US-11-370-301-11	Sequence 11, Appl
8	498	33.0	576	US-11-370-301-11	Sequence 11, Appl
9	498	33.0	610	US-10-948-737-13223	Sequence 13223, A
10	498	33.0	649	US-10-473-173-60	Sequence 60, Appl
11	498	33.0	658	US-11-282-283-3	Sequence 3, Appl
12	498	33.0	990	US-11-320-422-36	Sequence 36, Appl
13	498	33.0	990	US-11-346-596-3	Sequence 3, Appl
14	498	33.0	3542	US-11-349-727-9	Sequence 9, Appl
15	496.4	32.9	990	US-11-376-990-3	Sequence 3, Appl
16	494.8	32.8	3166	US-10-553-520-98	Sequence 98, Appl
17	494.8	32.8	3166	US-11-359-721-12	Sequence 12, Appl
18	494.8	32.8	3166	US-11-347-748-12	Sequence 12, Appl
19	443.2	29.4	541	US-11-266-748A-59044	Sequence 59044, A
20	441.2	29.3	600	US-10-956-160-2866	Sequence 2866, Ap
21	441.2	29.3	600	US-10-956-160-212973	Sequence 212973, A
22	416	27.6	648	US-11-021-541-3	Sequence 3, Appl

23	416	27.6	648	US-11-422-932-4	Sequence 4, Appl
24	416	27.6	648	US-11-422-947-4	Sequence 4, Appl
25	416	27.6	648	US-11-423-006-4	Sequence 4, Appl
26	416	27.6	1723	US-11-414-724-47	Sequence 47, Appl
27	416	27.6	1723	US-11-266-748A-29382	Sequence 29382, A
28	416	27.6	1723	US-11-339-733-61	Sequence 61, Appl
29	416	27.6	3614	US-11-349-727-11	Sequence 11, Appl
30	407.2	27.0	972	US-11-361-977A-61	Sequence 61, Appl
31	406	26.9	2848	US-11-320-422-42	Sequence 42, Appl
32	405.4	26.9	978	US-11-361-977A-62	Sequence 62, Appl
33	405	26.9	744	US-11-361-977A-64	Sequence 64, Appl
34	405	26.9	963	US-11-361-977A-58	Sequence 58, Appl
35	405	26.9	978	US-11-361-977A-52	Sequence 52, Appl
36	405	26.9	978	US-11-361-977A-55	Sequence 55, Appl
37	403.2	26.8	750	US-11-361-977A-65	Sequence 65, Appl
38	403.2	26.8	969	US-11-361-977A-53	Sequence 53, Appl
39	403.2	26.8	984	US-11-361-977A-56	Sequence 56, Appl
40	403.2	26.8	984	US-11-361-977A-56	Sequence 56, Appl
41	377.2	25.0	600	US-10-956-160-212974	Sequence 212974, A
42	377.2	25.0	654	US-10-956-160-2867	Sequence 2867, Ap
43	365	24.2	3665	US-11-349-727-13	Sequence 13, Appl
44	365	24.2	3665	US-11-323-964-25	Sequence 25, Appl
45	365	24.2	3665	US-11-323-964-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-11-177-646-413
; Sequence 413, Application US/11177646
; Publication No. US20060210967A1
; GENERAL INFORMATION:
; APPLICANT: AGAN, BRIAN
; APPLICANT: ROWLEY, ROBB
; APPLICANT: SETO, DONALD
; APPLICANT: STENGER, DAVID
; APPLICANT: THORNTON, JENNIFER
; APPLICANT: TIBBETTS, CLARK
; APPLICANT: THACH, DZUNG
; APPLICANT: VORA, GARY
; APPLICANT: WALTER, ELIZABETH
; APPLICANT: WANG, ZHENG
; TITLE OF INVENTION: RE-SEQUENCING PATHOGEN MICROARRAY
; FILE REFERENCE: AFD 735
; CURRENT APPLICATION NUMBER: US/11/177, 646
; PRIOR FILING DATE: 2005-07-02
; PRIOR FILING DATE: 07/02/04
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 413
; LENGTH: 948
; TYPE: DNA
; ORGANISM: E. coli 0157:H7, 32400301:1-948
US-11-177-646-413
Query Match 58.1%; Score 875.8; DB 10; Length 948;
Best local similarity 99.2%; Pred. No. 4.5e-270;
Matches 880; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 103 GATGTGAAGAAATTACCTTACCTTGCAGTSCAAGAGCGATGTGATTCGCTGAAT 162
DB 61 GTTCGAAGAAATTACCTTACCTTGCAGTSCAAGAGCGATGTGATTCCTGAAT 120
QY 163 GTCTTCGCTCTGCAATGAGTACCTCCATTACAGCTATTTTCATGAGAGGAGCTCTTTA 222
DB 121 GTCTTCGCTCTGCAATGAGTACCTCCATTACAGCTATTTTCATGAGAGGAGCTCTTTA 180
QY 223 CTGATGATTTGATGTGACGACAGGAGGATTAATTTGTTTCAGTTGATGTCAGAGGATGAT 282
DB 181 CTGATGATTTGATGTGACGACAGGAGGATTAATTTGTTTCAGTTGATGTCAGAGGATGAT 240

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QY 283 CCAGAGGAGGAGGGGTTTAATTAATCTACGGCTTAATGTTGAACGAATAATTAATATGTC 342
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QY 343 ACAGGATTTGTTAACAGGACAAATATGTTTTTATGCTTTGCTGATTTTTCATGTT 402
DB 301 ACAGGATTTGTTAACAGGACAAATATGTTTTTATGCTTTGCTGATTTTTCATGTT 360
QY 403 ACCCTTCAGATCAACAGCGGTTACATGTCGTGTCAGAGTACATTAACAGGTTACAG 462
DB 361 ACCCTTCAGATCAACAGCGGTTACATGTCGTGTCAGAGTACATTAACAGGTTACAG 420
QY 463 CGTGTTCAGAGGATCACTGTCGTAACGGGATCAGATTAATGCGCATTCGTTGACTACTT 522
DB 421 CGTGTTCAGAGGATCACTGTCGTAACGGGATCAGATTAATGCGCATTCGTTGACTACTT 480
QY 523 TATCTGATTTTAATGTCGATAGTGAACCTCAGTACGAGATCTGTGGCAAGGCGATG 582
DB 481 TATCTGATTTTAATGTCGATAGTGAACCTCAGTACGAGATCTGTGGCAAGGCGATG 540
QY 583 TTAAGGTTTGTACTGTCGAGCTGAAGCTTTACGTTTTCGGCAATATCAGAGGGGATTT 642
DB 541 TTAAGGTTTGTACTGTCGAGCTGAAGCTTTACGTTTTCGGCAATATCAGAGGGGATTT 600
QY 643 CGTACAACTGATGATGATCTCAAGTGGCGTTTATGTAATGACTGCTGAAGATGTTGAT 702
DB 601 CGTACAACTGATGATGATCTCAAGTGGCGTTTATGTAATGACTGCTGAAGATGTTGAT 660
QY 703 CTTACATTTGAACGCGGAGGTTGAGTACGCTGCTGCTGATCTATCTATGTAACAGACTCT 762
DB 661 CTTACATTTGAACGCGGAGGTTGAGTACGCTGCTGCTGATCTATCTATGTAACAGACTCT 720
QY 763 GTTCTGTAGAGAAATTTCTTTTGAAGCATTAATCAATCTGGGAAACGTTGACATTA 822
DB 721 GTTCTGTAGAGAAATTTCTTTTGAAGCATTAATCAATCTGGGAAACGTTGACATTA 780
QY 823 ATACTGATTTGATCATCATCATGATCGCGAGTTGCCAATGCGATCTGATGAGTTTCT 882
DB 781 ATACTGATTTGATCATCATCATGATCGCGAGTTGCCAATGCGATCTGATGAGTTTCT 840
QY 883 TCTATGTCGCGGAGATGAGAGTCCGCGGATTAACGACATTAATTAATTTGTTGGAT 942
DB 841 TCTATGTCGCGGAGATGAGAGTCCGCGGATTAACGACATTAATTAATTTGTTGGAT 900
QY 943 TCAATCCATCTCGGGGCAATTTCTGATCGCAGAACTATTAAGCAGTGG 989
DB 901 TCAATCCATCTCGGGGCAATTTCTGATCGCAGAACTATTAAGCAGTGG 947

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RESULT 2

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US-11-136-524-93
; Sequence 93, Application US/11136524
; Publication No. US20060094034A1
; GENERAL INFORMATION:
; APPLICANT: BROUSSEAU, Roland
; APPLICANT: HAREL, Josee
; APPLICANT: BEKAL, Sadjia
; TITLE OF INVENTION: ARRAY AND USES THEREOF
; FILE REFERENCE: 86369-3
; CURRENT APPLICATION NUMBER: US/11/136,524
; CURRENT FILING DATE: 2005-05-25
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-136-524-93

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Query Match 33.1%; Score 498.4; DB 8; Length 502;
Best Local Similarity 99.8%; Pred. No. 4,7e-149;
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 108 GAAGAAATTTACCTTAGACTTCTCGACTCAAAAGACGATATGATGCTGAATGTCAT 167
DB 3 GAAGAAATTTACCTTAGACTTCTCGACTCAAAAGACGATATGATGCTGAATGTCAT 62
QY 168 TGGCTCTGCAATAGTACTTCCATTACAGACTATTTTCATAGAGAGTACTCTTACTGAT 227
DB 63 TGGCTCTGCAATAGTACTTCCATTACAGACTATTTTCATAGAGAGTACTCTTACTGAT 122
QY 228 GATTATAGTGGCACAGGGGATTAATTTTTCAGTTGATGTCAGAGGATAGATCCAGA 287
DB 123 GATTATAGTGGCTCAGGGGATTAATTTTTCAGTTGATGTCAGAGGATAGATCCAGA 182
QY 288 GGAAGGCGGTTTAATTAATCTACCGCTTAATGTTGAACGAATTAATTAATGTCACAG 347
DB 183 GGAAGGCGGTTTAATTAATCTACCGCTTAATGTTGAACGAATTAATTAATGTCACAG 242
QY 348 ATTTGTTAACAGACAAATTAATGTTTTTATGCTTGTGATTTTTCATGTTACCTT 407
DB 243 ATTTGTTAACAGACAAATTAATGTTTTTATGCTTGTGATTTTTCATGTTACCTT 302
QY 408 TCCAGGTACAAAGCGGTTTACATTTGTCGTGACAGTACTATACACGTTACAGCGTGT 467
DB 303 TCCAGGTACAAAGCGGTTTACATTTGTCGTGACAGTACTATACACGTTACAGCGTGT 362
QY 468 TCGAGGATCACTGTCGTAACGGGATGCAATTAATGCGCAATGCTGACTACTTCTATCT 527
DB 363 TCGAGGATCACTGTCGTAACGGGATGCAATTAATGCGCAATGCTGACTACTTCTATCT 422
QY 528 GGATTTAATGTCGATAGTGAACCTCACTGACGAGCTGTGGCAAGCGGATGTTAG 587
DB 423 GGATTTAATGTCGATAGTGAACCTCACTGACGAGCTGTGGCAAGCGGATGTTAG 482
QY 588 GTTTGTACTGTGACAGCTG 607
DB 483 GTTTGTACTGTGACAGCTG 502

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RESULT 3

```

US-11-021-541-2
; Sequence 2, Application US/11021541
; Publication No. US20060287259A1
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; APPLICANT: TOLENTINO, MICHAEL J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DBR-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-021-541-2

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Query Match 33.0%; Score 498; DB 7; Length 576;
Best Local Similarity 100.0%; Pred. No. 6,9e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1010 GCACCCATGCGCAGAGAGGAGGCGAATCATCATCAGAAAGTGTGAAGTTCATGATGTC 1069
DB 79 GCACCCATGCGCAGAGAGGAGGCGAATCATCATCAGAAAGTGTGAAGTTCATGATGTC 138
QY 1070 TATCAGCGCAGCTACCTGATCCATTCATGAGACCTCTGTGGACATCTTCAGAGGTAACCT 1129
DB 139 TATCAGCGCAGCTACCTGATCCATTCATGAGACCTCTGTGGACATCTTCAGAGGTAACCT 198
QY 1130 GATGAGATCGAGTACATCTTCAAGCAGCTCTGTGTCCTGTCATGTCGATGCGGAGGCTG 1189
DB 199 GATGAGATCGAGTACATCTTCAAGCAGCTCTGTGTCCTGTCATGTCGATGCGGAGGCTG 258

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QY 1190 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGTCCAAATCATCATGAGATT 1249
| | | | |
Db 259 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGTCCAAATCATCATGAGATT 318
| | | | |
QY 1250 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTACAGCAAC 1309
| | | | |
Db 319 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTACAGCAAC 378
| | | | |
QY 1310 AAATGTGAATGACGACCAAGAAAGATAGACGAAAGAAATCCCTGTGGGCGCTTGC 1369
| | | | |
Db 379 AAATGTGAATGACGACCAAGAAAGATAGACGAAAGAAATCCCTGTGGGCGCTTGC 438
| | | | |
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCCGACAGTGTAAATGTTCTTCAAA 1429
| | | | |
Db 439 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCCGACAGTGTAAATGTTCTTCAAA 498
| | | | |
QY 1430 AACACGACTCCGCTTGCAAGCGGAGGAGCTTGAGTTAAACGACGTACTTGACAGAT 1489
| | | | |
Db 499 AACACGACTCCGCTTGCAAGCGGAGGAGCTTGAGTTAAACGACGTACTTGACAGAT 558
| | | | |
QY 1490 GACAAAGCGAGGCGGTGA 1507
| | | | |
Db 559 GACAAAGCGAGGCGGTGA 576
| | | | |

RESULT 4

US-11-422-932-3
; Sequence 3, Application US/11422932
; Publication No. US20060286073A1
; GENERAL INFORMATION:
; APPLICANT: Tolentino, Michael J.
; APPLICANT: Reich, Samuel Jotham
; TITLE OF INVENTION: Compositions and Methods for siRNA
; FILE REFERENCE: 43826-1
; CURRENT APPLICATION NUMBER: US/11/422,932
; CURRENT FILING DATE: 2006-06-08
; PRIOR APPLICATION NUMBER: US/10/294,228
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/398,417
; PRIOR FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-422-932-3

Query Match 33.0%; Score 498; DB 7; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.9e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGAGGAGGAGATCATCATGAGAGTGTGAATTCATGATGTC 1069
| | | | |
Db 79 GCACCCATGCGAGAGAGAGAGGAGGAGATCATCATGAGAGTGTGAATTCATGATGTC 138
| | | | |
QY 1070 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGTGAGACATCTTCAGAGTAACCT 1129
| | | | |
Db 139 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGTGAGACATCTTCAGAGTAACCT 198
| | | | |
QY 1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCGCTGATGCGAGTGC 1189
| | | | |
Db 199 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCGCTGATGCGAGTGC 258
| | | | |
QY 1199 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 1249
| | | | |
Db 259 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 318
| | | | |
QY 1250 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTACAGCAAC 1309
| | | | |
Db 319 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTACAGCAAC 378
| | | | |

QY 1310 AAATGTGAATGACGACCAAGAAAGATAGACGAAAGAAATCCCTGTGGGCGCTTGC 1369
| | | | |
Db 379 AAATGTGAATGACGACCAAGAAAGATAGACGAAAGAAATCCCTGTGGGCGCTTGC 438
| | | | |
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCCGACAGTGTAAATGTTCTTCAAA 1429
| | | | |
Db 439 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCCGACAGTGTAAATGTTCTTCAAA 498
| | | | |
QY 1430 AACACGACTCCGCTTGCAAGCGGAGGAGCTTGAGTTAAACGACGTACTTGACAGAT 1489
| | | | |
Db 499 AACACGACTCCGCTTGCAAGCGGAGGAGCTTGAGTTAAACGACGTACTTGACAGAT 558
| | | | |
QY 1490 GACAAAGCGAGGCGGTGA 1507
| | | | |
Db 559 GACAAAGCGAGGCGGTGA 576
| | | | |

RESULT 5

US-11-422-947-3
; Sequence 3, Application US/11422947
; Publication No. US20060292120A1
; GENERAL INFORMATION:
; APPLICANT: Tolentino, Michael J.
; APPLICANT: Reich, Samuel Jotham
; TITLE OF INVENTION: Compositions and Methods for siRNA
; FILE REFERENCE: 43826-1
; CURRENT APPLICATION NUMBER: US/11/422,947
; CURRENT FILING DATE: 2006-06-08
; PRIOR APPLICATION NUMBER: US/10/294,228
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/398,417
; PRIOR FILING DATE: 2002-07-24
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-422-947-3

Query Match 33.0%; Score 498; DB 7; Length 576;
Best Local Similarity 100.0%; Pred. No. 6.9e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGCGAGAGAGAGGAGGAGATCATCATGAGAGTGTGAATTCATGATGTC 1069
| | | | |
Db 79 GCACCCATGCGAGAGAGAGGAGGAGATCATCATGAGAGTGTGAATTCATGATGTC 138
| | | | |
QY 1070 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGTGAGACATCTTCAGAGTAACCT 1129
| | | | |
Db 139 TATCAGCGGAGCTACTGCGCATCATCGAGACCTGTGTGAGACATCTTCAGAGTAACCT 198
| | | | |
QY 1130 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCGCTGATGCGAGTGC 1189
| | | | |
Db 199 GATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCGCTGATGCGAGTGC 258
| | | | |
QY 1199 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 1249
| | | | |
Db 259 TGCATGACGAGGCGCTGAGTGTGTGCCCACTGAGAGATCCAAATCATCATGAGATT 318
| | | | |
QY 1250 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTACAGCAAC 1309
| | | | |
Db 319 ATGCGGATCAAACTTCACCAAGGCCAGCATATGAGAGATGAGTCTTCTACAGCAAC 378
| | | | |
QY 1310 AAATGTGAATGACGACCAAGAAAGATAGACGAAAGAAATCCCTGTGGGCGCTTGC 1369
| | | | |
Db 379 AAATGTGAATGACGACCAAGAAAGATAGACGAAAGAAATCCCTGTGGGCGCTTGC 438
| | | | |
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCCGACAGTGTAAATGTTCTTCAAA 1429
| | | | |
Db 439 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCCGACAGTGTAAATGTTCTTCAAA 498
| | | | |

Db 496 AACACAGACTCGCGTTCAGAAAGCGAGCGAGCTTGAGTTAAACGAAGTACTTGACAGATGT 555
QY 1490 GACACAGCCGAGGCGGTGA 1507
Db 556 GACAAAGCCGAGGCGGTGA 573

RESULT 10

US-10-473-173-60
; Sequence 60, Application US/10473173
; Publication No. US200608823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-60

Query Match 33.0%; Score 498; DB 6; Length 649;
Best Local Similarity 100.0%; Pred. No. 7.5e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCAACCATGCGACAGAGAGGCGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 1069
Db 95 GCACCCATGCGACAGAGAGGCGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 154
QY 1070 TATCAGCGCAGCTACTGCTCCATCCATCGAGACCCCTGGTGACATCTTCAGAGTACCT 1129
Db 155 TATCAGCGCAGCTACTGCTCCATCCATCGAGACCCCTGGTGACATCTTCAGAGTACCT 214
QY 1130 GATGAGATCGAGTACATCTTCAGAGCCATCTGTCGCTCCGATGCGATGCGGCGCTGC 1189
Db 215 GATGAGATCGAGTACATCTTCAGAGCCATCTGTCGCTCCGATGCGATGCGGCGCTGC 274
QY 1190 TGCAGATGCGAGGCGCTGAGTGTGTGCGCCACTGAGAGTCCAAATCACCATGCAAT 1249
Db 275 TGCAGATGCGAGGCGCTGAGTGTGTGCGCCACTGAGAGTCCAAATCACCATGCAAT 334
QY 1250 ATGCGGATCAAACTCCACCAAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 1309
Db 335 ATGCGGATCAAACTCCACCAAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 394
QY 1310 AAATGTGAATGCGACCAACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGGGCGCTTCG 1369
Db 395 AAATGTGAATGCGACCAACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGGGCGCTTCG 454
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGACAGCTGTAAATGTTCTCTGAAA 1429
Db 455 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGACAGCTGTAAATGTTCTCTGAAA 514
QY 1430 AACACAGACTCGCGTTCAGAAAGCGAGCGAGCTTGAGTTAAACGAAGTACTTGACAGAT 1489
Db 515 AACACAGACTCGCGTTCAGAAAGCGAGCGAGCTTGAGTTAAACGAAGTACTTGACAGAT 574
QY 1490 GACAAAGCCGAGGCGGTGA 1507
Db 575 GACAAAGCCGAGGCGGTGA 592

RESULT 11
US-11-282-283-3
; Sequence 3, Application US/11282283

; Publication No. US20060141627A1
; GENERAL INFORMATION:
; APPLICANT: Comer, Allen
; TITLE OF INVENTION: Vectors for Stable Gene Expression
; FILE REFERENCE: SPATA-10492
; CURRENT APPLICATION NUMBER: US/11/282,283
; CURRENT FILING DATE: 2005-11-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-282-283-3

Query Match 33.0%; Score 498; DB 9; Length 658;
Best Local Similarity 100.0%; Pred. No. 7.5e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCAACCATGCGACAGAGAGGCGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 1069
Db 81 GCACCCATGCGACAGAGAGGCGAGATCATCAGAACTGGTGAAGTTTCATGATGTC 140
QY 1070 TATCAGCGCAGCTACTGCTCCATCCATCGAGACCCCTGGTGACATCTTCAGAGTACCT 1129
Db 141 TATCAGCGCAGCTACTGCTCCATCCATCGAGACCCCTGGTGACATCTTCAGAGTACCT 200
QY 1130 GATGAGATCGAGTACATCTTCAGAGCCATCTGTCGCTCCGATGCGATGCGGCGCTGC 1189
Db 201 GATGAGATCGAGTACATCTTCAGAGCCATCTGTCGCTCCGATGCGATGCGGCGCTGC 260
QY 1190 TGCAGATGCGAGGCGCTGAGTGTGTGCGCCACTGAGAGTCCAAATCACCATGCAAT 1249
Db 261 TGCAGATGCGAGGCGCTGAGTGTGTGCGCCACTGAGAGTCCAAATCACCATGCAAT 320
QY 1250 ATGCGGATCAAACTCCACCAAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 1309
Db 321 ATGCGGATCAAACTCCACCAAGGCGAGACATAGAGAGATGAGCTTCTTACAGCACAC 380
QY 1310 AAATGTGAATGCGACCAACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGGGCGCTTCG 1369
Db 381 AAATGTGAATGCGACCAACCAAGAAAGATAGAGCAAGAAAGAAATCCCTGGGCGCTTCG 440
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGACAGCTGTAAATGTTCTCTGAAA 1429
Db 441 TCAGAGCGGAGAAAGCATTTGTTGTACAAGATCCGACAGCTGTAAATGTTCTCTGAAA 500
QY 1430 AACACAGACTCGCGTTCAGAAAGCGAGCGAGCTTGAGTTAAACGAAGTACTTGACAGAT 1489
Db 501 AACACAGACTCGCGTTCAGAAAGCGAGCGAGCTTGAGTTAAACGAAGTACTTGACAGAT 560
QY 1490 GACAAAGCCGAGGCGGTGA 1507
Db 561 GACAAAGCCGAGGCGGTGA 578

RESULT 12

US-11-320-422-36
; Sequence 36, Application US/11320422
; Publication No. US20060154285A1
; GENERAL INFORMATION:
; APPLICANT: Leung, Tinchung
; APPLICANT: Robishaw, Janet D.
; TITLE OF INVENTION: Zebrafish Heterotrimer G-Protein Gamma 2 Subunit (GNM2)
; FILE REFERENCE: GEIS-0014
; CURRENT APPLICATION NUMBER: US/11/320,422
; CURRENT FILING DATE: 2005-12-28
; PRIOR APPLICATION NUMBER: US 60/640,802
; PRIOR FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 990

TYPE: DNA
ORGANISM: Homo sapiens
US-11-320-422-36

Query Match 33.0%; Score 498; DB 9; Length 990;
Best Local Similarity 100.0%; Pred. No. 9.9e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAAATGTGAGATTCATGATGTC 1069
DB 135 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAAATGTGAGATTCATGATGTC 194
QY 1070 TATCAGGCGAGCTACTGTCATTCATCGAGACCTGTGTGATCATCTTCAGAGTACCT 1129
DB 195 TATCAGGCGAGCTACTGTCATTCATCGAGACCTGTGTGATCATCTTCAGAGTACCT 254
QY 1130 GATGAGATCGAGTACATCTTCAGAGCTGTGTGATCATCTTCAGAGTACCT 1249
DB 255 GATGAGATCGAGTACATCTTCAGAGCTGTGTGATCATCTTCAGAGTACCT 314
QY 1190 TGCAATGACGAGGCGCTGAGTGTGTGATCATCTTCAGAGTACCT 1369
DB 315 TGCAATGACGAGGCGCTGAGTGTGTGATCATCTTCAGAGTACCT 494
QY 1250 ATGCGGATCAAACTCTCAGCAAGGCGAGCATAGAGAGATGAGCTTCTACAGACAC 1309
DB 375 ATGCGGATCAAACTCTCAGCAAGGCGAGCATAGAGAGATGAGCTTCTACAGACAC 434
QY 1310 AAATGTGATGACAGACCAAGAAAGATGAGAGACAGCAAGAAATCCTGTGGGCTTGC 1369
DB 435 AAATGTGATGACAGACCAAGAAAGATGAGAGACAGCAAGAAATCCTGTGGGCTTGC 494
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCGACAGCTGTAATGTTCTGCAAA 1429
DB 495 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCGACAGCTGTAATGTTCTGCAAA 554
QY 1430 AACACAGACTCGCTGTCGAAAGCGAGGAGCTTGAGTTAAAGAGTATTCGAGATGT 1489
DB 555 AACACAGACTCGCTGTCGAAAGCGAGGAGCTTGAGTTAAAGAGTATTCGAGATGT 614
QY 1490 GACAAGCCGAGGCGGTGA 1507
DB 615 GACAAGCCGAGGCGGTGA 632

RESULT 13

US-11-346-596-3
Sequence 3, Application US/11346596
Publication No. US20060188503A1
GENERAL INFORMATION:
APPLICANT: Shen, Ben-Quan
APPLICANT: Zioncheck, Thomas
TITLE OF INVENTION: MODULATION OF ENOS ACTIVITY AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P17351
CURRENT APPLICATION NUMBER: US/11/346,596
CURRENT FILING DATE: 2006-02-02
PRIOR APPLICATION NUMBER: US/09/700,806
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: PCT/US00/30294
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/163,132
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTH: 990
TYPE: DNA
ORGANISM: Homo sapiens
US-11-346-596-3

Query Match 33.0%; Score 498; DB 10; Length 990;
Best Local Similarity 100.0%; Pred. No. 9.9e-149;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1010 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAAATGTGAGATTCATGATGTC 1069
DB 135 GCACCCATGGCAGAGAGAGAGAGAGATCATCAGAAATGTGAGATTCATGATGTC 194
QY 1070 TATCAGGCGAGCTACTGTCATTCATCGAGACCTGTGTGATCATCTTCAGAGTACCT 1129
DB 195 TATCAGGCGAGCTACTGTCATTCATCGAGACCTGTGTGATCATCTTCAGAGTACCT 254
QY 1130 GATGAGATCGAGTACATCTTCAGAGCTGTGTGATCATCTTCAGAGTACCT 1249
DB 255 GATGAGATCGAGTACATCTTCAGAGCTGTGTGATCATCTTCAGAGTACCT 314
QY 1190 TGCAATGACGAGGCGCTGAGTGTGTGATCATCTTCAGAGTACCT 1369
DB 315 TGCAATGACGAGGCGCTGAGTGTGTGATCATCTTCAGAGTACCT 494
QY 1250 ATGCGGATCAAACTCTCAGCAAGGCGAGCATAGAGAGATGAGCTTCTACAGACAC 1309
DB 375 ATGCGGATCAAACTCTCAGCAAGGCGAGCATAGAGAGATGAGCTTCTACAGACAC 434
QY 1310 AAATGTGATGACAGACCAAGAAAGATGAGAGACAGCAAGAAATCCTGTGGGCTTGC 1369
DB 435 AAATGTGATGACAGACCAAGAAAGATGAGAGACAGCAAGAAATCCTGTGGGCTTGC 494
QY 1370 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCGACAGCTGTAATGTTCTGCAAA 1429
DB 495 TCAGAGCGGAGAAAGCATTTGTTGTACAAATCCGACAGCTGTAATGTTCTGCAAA 554
QY 1430 AACACAGACTCGCTGTCGAAAGCGAGGAGCTTGAGTTAAAGAGTATTCGAGATGT 1489
DB 555 AACACAGACTCGCTGTCGAAAGCGAGGAGCTTGAGTTAAAGAGTATTCGAGATGT 614
QY 1490 GACAAGCCGAGGCGGTGA 1507
DB 615 GACAAGCCGAGGCGGTGA 632

RESULT 14

US-11-349-727-9
Sequence 9, Application US/11349727
Publication No. US20070009484A1
GENERAL INFORMATION:
APPLICANT: HUNT, KELLY K.
APPLICANT: SUH, YOUNG-JIN
APPLICANT: SWISHER, STEPHEN G.
APPLICANT: PATNER, ABUTJANG
APPLICANT: RAMESH, RAJAGOPAL
APPLICANT: SHANKER, MANISH
TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING MDA-7 FOR THE
TITLE OF INVENTION: TREATMENT OF CANCER
FILE REFERENCE: UTSC:924US/INGN:13305
CURRENT APPLICATION NUMBER: US/11/349,727
CURRENT FILING DATE: 2006-02-08
PRIOR APPLICATION NUMBER: 60/650,807
PRIOR FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: 60/661,679
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: 60/676,096
PRIOR FILING DATE: 2005-04-29
PRIOR APPLICATION NUMBER: 60/749,372
PRIOR FILING DATE: 2005-12-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 3542
TYPE: DNA
ORGANISM: Homo sapiens
US-11-349-727-9

Query Match 33.0%; Score 498; DB 7; Length 3542;
Best Local Similarity 100.0%; Pred. No. 2.3e-148;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	195	TATCAGGCGAGCTACTGCAATCCAAATGGAGACCCCTGGGAGCATCTTCCAGGATACCCT	254
Qy	1130	GATGAGATTCGAGTACATCTTTCAAGCCATCTCTGTGCCCCCTGATGCCATGGGGGGGCTGC	1188
Db	255	GATGAGATTCGAGTACATCTTCCAAACCAATCTCTGTGCCCCCTGATGCCAGATGGGGGGGCTGC	314
Qy	1190	TGCATATGACGAGGAGCTGGAGTGTGTGCGCCACTGAGAGAGTCCAACATCAACATGCAGATT	1244
Db	315	TGCATATGACGAGGAGCTGGAGTGTGTGCGCCACTGAGAGAGTCCAACTCAACATGCAGATT	374
Qy	1250	ATGCGGATCCAAACCTCACCAAGGCCGAGCACAATGAGAGATGAGCTTCTTACAGCACAAC	1304
Db	375	ATGCGGATCCAAACCTCACCAAGGCCGAGCACAATGAGAGATGAGCTTCTTACAGCACAAC	434
Qy	1310	AAATGTAAATCCAAACCAAGAAAGATGAGACCAAGACAAAGAAATCCCTGGGGGCTTGC	1364
Db	435	AAATGTAAATCCAAACCAAGAAAGATGAGACCAAGACAAAGAAATCCCTGGGGGCTTGC	494
Qy	1370	TCAGAGCGAGAAAGACATTTGTTGTACAAAGATCGCAGACGTGTAAATGTTCTTGCAAA	1422
Db	495	TCAGAGCGAGAAAGACATTTGTTGTACAAAGATCGCAGACGTGTAAATGTTCTTGCAAA	554
Qy	1430	AAACAAGACTCGCGTTGCAAGGCGAGGACGCTTGATTAACGAACGTACTTGCAGATGT	1488
Db	555	AAACAAGACTCGCGTTGCAAGGCGAGGACGCTTGATTAACGAACGTACTTGCAGATGT	614
Qy	1490	GACAAGCGAGGCGGTGA 1507	
Db	615	GACAAGCGAGGCGGTGA 632	